

THE INDIAN HUMAN HERITAGE

Editors

**D Balasubramanian
N Appaji Rao**



THE INDIAN HUMAN HERITAGE

THE INDIAN HUMAN HERITAGE

Editors

D Balasubramanian

N Appaji Rao



Universities Press

Universities Press (India) Limited

Registered Office

3-5-819 Hyderguda, Hyderabad 500 029 (A.P.), India

Distributed by

Orient Longman Limited

Registered Office

3-6-272 Himayatnagar, Hyderabad 500 029 (A.P.), India

Other Offices

Bangalore / Bhopal / Bhubaneshwar / Calcutta / Chennai

Ernakulam / Guwahati / Hyderabad / Jaipur

Lucknow / Mumbai / New Delhi / Patna

© Universities Press (India) Limited 1998

First published 1998

ISBN 81 7371 128 3

Typesetting and figures by

AICRA Info Mates Pvt. Ltd., Hyderabad 500 020

Printed in India at

Vinayaka Sai Offset Printers, Hyderabad 500 004

Published by

Universities Press (India) Limited

3-5-819 Hyderguda, Hyderabad 500 029

Contents

<i>Preface</i>	vii
<i>Presidential remarks</i>	ix
1 Genes and environment as determinants of health and disease <i>V. Ramalingaswami</i>	1
2 β -Thalassemia in India—Molecular biology to community control of this blood disease <i>I.C. Verma, R. Saxena</i>	4
3 Consanguinity—A common human heritage? The effects on the health and well-being of Indian populations <i>N. Appaji Rao, H.S. Savithri, A. Radha Rama Devi, A.H. Bittles</i>	11
4 Human health and our heritage <i>P.N. Tandon</i>	22
5 Molecular genetic markers in the study of human heritage <i>Shama Barnabas, C.G. Suresh</i>	27
6 People of India: Biological diversity and affinities <i>Partha P. Majumder</i>	45
7 Contribution of geochronology to Indian human heritage <i>S. Mishra, S.N. Rajaguru, B.L.K. Somayajulu</i>	60
8 Rapid climatic shifts and its influence on ancient civilisations: Evidence from marine records <i>Pothuri Divakar Naidu</i>	69
9 The people of India: Diversities and linkages <i>K.S. Singh</i>	78
10 The Indian heritage – A sociological perspective <i>André Bêteille</i>	87

11	The language heritage of India <i>D.P. Pattanayak</i>	95
12	Peopling of India <i>Madhav Gadgil, N.V. Joshi, U.V. Shambu Prasad, S. Manoharan, Suresh Patil</i>	100
	<i>Contributors and editors</i>	130
	<i>Index</i>	134

Preface

Friends,

On behalf of the Indian National Science Academy (INSA) I have pleasure in presenting the edited proceedings of the one-and-a-half-day symposium entitled “The Indian Human Heritage”. The genesis of this heritage symposium lies squarely with Dr. Sudha Gangal who suggested that we might consider a symposium on the genetic aspects of the Indian population. We tossed that idea around a little in the Council and then expanded the theme to include the entire heritage—not just the genetic heritage but also the anthropological heritage, the medical and health aspects, archaeological findings, sociological, linguistic and, where possible, even certain aspects of culture, such as music, and so on. As you would notice, it sweeps quite a broad canvas, and I have been particularly helped in this by Dr. Lotika Varadarajan who has been suggesting and advising me on a variety of topics and people, experts and so on. It is thus that we are going to have a day-and-a-half of what might be the Indian human heritage approached from the medical and health aspects, the genetic aspect or genetic heritage (taking us right on to our DNA and molecular tree as far back as we can); the archaeological aspects where we look at not only the techniques of dating archaeological material, but also assess the changes that have happened to the climatic and the geological conditions in the Indian subcontinent and their effect on our own human heritage including the Harappan and Indus Valley civilisations, and anthropological aspects.

We are particularly happy and fortunate that participants include stalwarts like Dr. K.S. Singh, who has been the main force behind the compilation of the magnificent volumes called *The People of India*, Prof. André Béteille of Delhi University who will tell us about the social aspects of Indian Heritage and Dr. D. P. Pattanayak, the Founder-Director of the Central Institute of Indian Languages who will take us through the language heritage of India.

Dr. Appaji Rao and I are thought to be the conveners, but we are only the front people. There has been a lot of backroom work that has been done not only by Dr. Varadarajan and Mrs. Varadarajan but also a number of others, notably Prof. Sharat Chandra, Prof. Ramalingaswami and Prof. Tandon. A book on a subject like this has not, to my knowledge, been attempted before, by any academy in India. With these words may I invite our President, Dr. Varadarajan, to express his presidential remarks, as well as remarks about the symposium itself.

D. Balasubramanian (Convener)

Director, Centre for Cellular and Molecular Biology, Hyderabad

Presidential remarks

It is indeed a memorable day. This symposium is really an extraordinary new step. I welcome the presence of three of our former presidents—a source of great encouragement to us—and a very large number of Fellows of the Academy as well as those who are connected with social sciences in many ways and who are leaders in their respective fields. The objectives of the Academy set forth by the founders clearly state that our purpose in founding the Academy is to promote Science and use it for the benefit of humanity. We therefore wanted to use the vast talent in this country and our rich knowledge of our ancient traditions in a fitting manner—one such expression has come through the strengthening of the activities of the Indian National Commission of the History of Science. This is an extremely valuable and unique organization, the management of which is entrusted to the Academy. And it is one occasion where we are constantly enriched by the presence of distinguished historians, the richness of their thoughts and the wealth of materials they possess—not only in English but in many Asian, European and other languages. This has resulted in a number of valuable publications and the journal is now very active. We hope to strengthen it and invite many more people to participate. I believe we particularly need participation and writing about what we call the modern period. Since the last 150 years there have been many advances but we are losing the records of many institutions, of many of our founders and distinguished members of the scientific community. So I am using this occasion to appeal to you to identify persons who will be interested in producing monographs or even making available their manuscripts and collections. We owe it to the very heritage and tradition which our founders imposed on themselves not to lose that commitment. Another area we have therefore looked at is the general programme, which I think was instituted sometime ago with Prof. Tandon, Prof. Joshi and Prof. Sharma to look at the area we can call Science and Society. We have now been making some attempts to look at those areas which are of great concern to readers in this country, to the public at large and therefore the release of the book on *Biodiversity and Sustainable Development* by the respected Rashtrapatiiji is again an indication of our concern about a very important area. We have also held other important seminars. We have had one on “Advances in Information Technology” and its impact on us. We have had an exhibition and had produced something on information technology, especially on science and technology communication which was held in March and which we are attempting to publish. We have similarly one in May on “Intellectual Property Rights in Biology”. The proceedings of that meeting are now ready and will be published very soon. Similarly we have others, an important one being on “Sustaining and Attracting Scientific Talent” which is an area in which we are facing a great crisis. Now many young people are finding it difficult to continue their career in science since there are so many other attractions. We

are hoping to do much work in this area and that will also result in a publication. Emboldened by these experiments, we decided to take steps, take risks and possibly fail. But if you do not take risks you cannot succeed. So we must do something that is not easily possible, which is not impossible but nearly impossible. And this symposium on “Human Heritage” is ambitious in the sense that it is an original idea, a voyage of discovery, which promises to give us new insights and a new understanding of what is human. One of the reasons for choosing this subject at this time is that advances in science and technology are making it possible to establish who you are. We know how to answer that. “I am so and so”. But beyond that, what are you? What are you made up of? Why are you made up of it?

The path to understanding the nature of the universe and the nature of human forces is full of mystery. But it is this attempt which will lead us along the very ambitious ideals of our founders—that we should see how science can explore and be beneficial. Because of the rapidity with which interactions now take place in the world, much of what we call “human heritage”, which takes centuries or even eons to build up, is being invaded by other forces and is lost. So this word “sustainable development” has not only to do with physical forces, nature and materials, but also our cultural and other activities which are far more difficult to create.

I must compliment all those who have been involved in organising this Symposium and in bringing together extraordinary people, each one with great concern for society, and I think this Academy, the Symposium and this whole auditorium will echo and be enriched by their voices and thoughts. We hope this new beginning will produce many more such events and I hope many of the speakers will not only talk about what they are now doing, but share their knowledge and suggest to us and the Academy new topics, new methods of exploration, may be sub-workshops, and many new forms. I wish the symposium every success. I will watch it with great interest because it is going to illuminate our thinking and our philosophy, and if we absorb a little of it and convey it to our other generations, younger people will benefit a great deal. Our ambition is to cover four major themes next year and publish the proceedings. The Academy will provide all facilities. I request all of you to send in your papers in the next two to three weeks before you get busy with other activities. We will help you in recording and presenting your papers using the modern instrumentation facilities at the Academy. The response has been good and I hope it will be a great success on which to base our future activities. I thank you, Dr. Balasubramanian and Dr. Appaji Rao, for giving me this opportunity to share my joy, my interest, and my expectations from all of you. Thank you.

Dr. S. Varadarajan
President, Indian National Science Academy (INSA), New Delhi

1

Genes and environment as determinants of health and disease

V. Ramalingaswami

Department of Pathology, All India Institute of Medical Sciences, New Delhi

Introduction

We may agree with Alexander Pope that the proper study of man is man himself, leading to man's understanding of man. The Oracle of Delphi advised man: "know thyself". In this setting, the human genome is fundamental but it does not represent the totality. There is an interplay of social, cultural, dietary, genetic and other factors that provide the backdrop over the flux of time to a vision of Human Heritage. Destiny is more than genes; changes in diet are just as much biological determinants as genetics. This Seminar is about understanding Indian human heritage in its composite sense and may provide clues to the pressing biological, social and cultural questions of today. The first session is devoted to health issues.

Isolation, migration, immigration, amalgamation and assimilation of populations are phenomena that underlie human heritage over time. They, in turn, are influenced by geographic, biological and social factors or by the intervention of man himself. These lead to a number of genetic situations. Geographic isolation reduces gene flows. Isolation is of many types—geographic, ecological, mechanical and social. In the modern world, geographic isolation is being breached in a profound way through increases in the speed and modes of travel.

Migration

Migration is a powerful influence on minority communities, with their own genetic and environmental influences, producing in them unique disease profiles. Travel of humans, vectors and animals across continents is profoundly influenced by the technological change in the speed and ease of travel; jet travel has replaced the steamship in the spread of disease and disease vectors. The story of plague and the successive pandemics around the world are of interest in this connection. The first pandemic of plague is depicted in Fig. 1. The green areas are from AD 541 to AD 544, and the shaded areas represent the period AD 557–567, when 14 successive epidemics of plague had taken place. Possibly like the archetypal man himself, plague had originated in Africa and moved in the two directions shown in the figure, just as early man had actually moved. Figure 2 is yet another chapter in the story of plague and man. The second pandemic of

plague had occurred in the 13th–14th centuries and the arrows in the figure show the movement of plague at that time. Figure 3 illustrates the third pandemic of plague commencing in the 1850s, influenced by the steamship, which had been invented by that time. The movement of people and goods along rivers, seas and oceans led to the dissemination of plague in an extraordinary manner. The picture of migration on this planet is well exemplified by plague. Each society by its history, degree of isolation—its own dynamics—influences the transmission and expression of genotypes and the distribution of alleles.

The story of Asian immigrants to the UK, South Africa and Fiji, and the high frequency with which coronary artery disease, hypertension, insulin resistance and hypertriglyceridaemia manifest in them in comparison with the local population is now well documented, bringing out forcefully the ‘nature–nurture’ interaction. The high frequency of gastric cancer in first generation Japanese immigrants to the USA and its gradual fall in succeeding generations is another forceful epidemiological factor illustrating the ‘nature–nurture’ interaction. Common diseases as opposed to the rare single gene disorders of Mendelian pattern are not determined at fertilisation by single gene defects or chromosomal abnormalities; they are attributable to the interaction between multiple genetic and environmental influences. Non-communicable diseases are believed to have arisen from exposure to the conditions of life for which man is genetically ill-equipped. Figure 4 shows the complex interaction of heredity and environment in Type II diabetes mellitus.

Non-communicable diseases

As far as Indian human heritage is concerned, non-communicable diseases are major and powerful influences determining adult mortality and morbidity. This extends not only to communicable diseases but also into areas of human behaviour. We know for example that on chromosome 6 sit a number of possible loci associated with schizophrenia (Fig. 5). So we are entering a territory where genes interacting among themselves, and the genomes interacting with the environment produce a kaleidoscopic picture of human heritage. A question that can be asked as a result of these studies is whether criminal behaviour is merely a question of transgression of the laws of the land or is it something that is determined by genetic elements?

Infectious diseases – malaria and HIV

I would now like to reflect briefly on the evolution of infectious diseases in relation to the human genome. Malaria in relation to human destiny and human genome is a fascinating chapter in the evolution of man. Figure 6 shows Angkor Vat, the great temple of Cambodia. It took a long time (from the 9th to the 12th century) to build and to complete. Waves of people came from surrounding areas and perished in the marshy grounds around Angkor Vat due to malaria caused by the parasite *Plasmodium falciparum*. Figure 7 shows one of the images inside Angkor Vat, depicting the worship of Vishnu and Vishnu formats, indicating the churning of the sea.

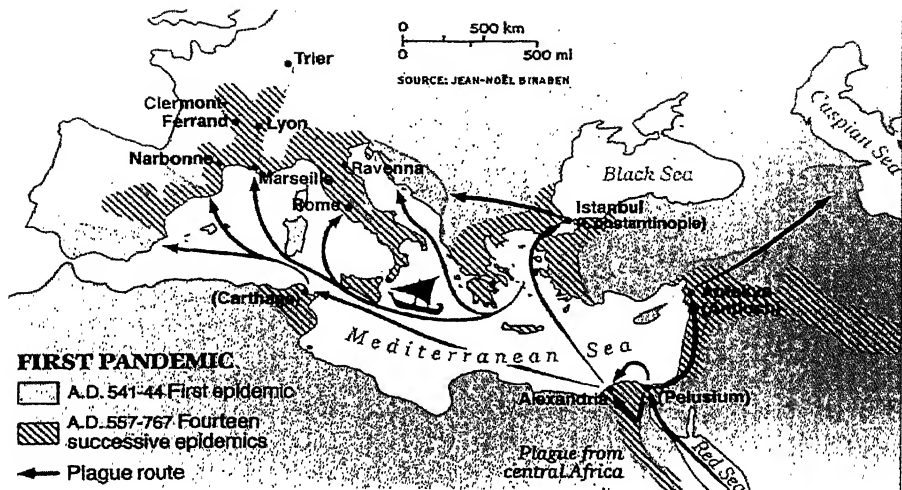


Fig.1 The first pandemic spread of plague from its origin in tropical Africa, that occurred in waves during the 6th century AD.

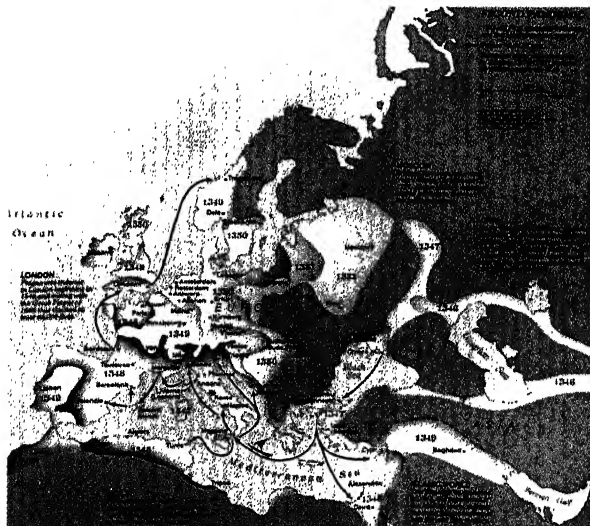


Fig.2 The second pandemic of plague of the 13th and 14th centuries

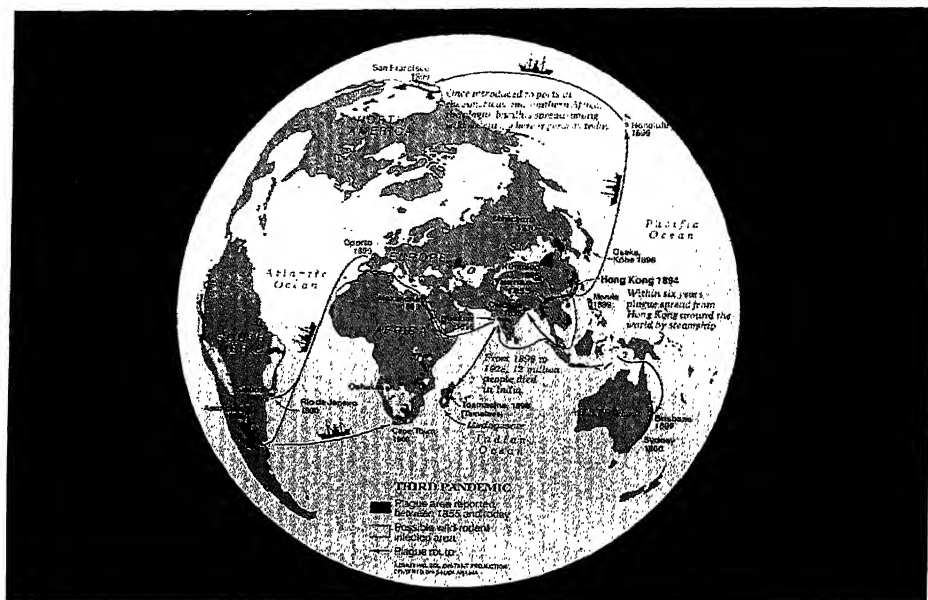


Fig.3 The third pandemic of plague of the mid-19th century spread faster and wider as a result of steamship travel

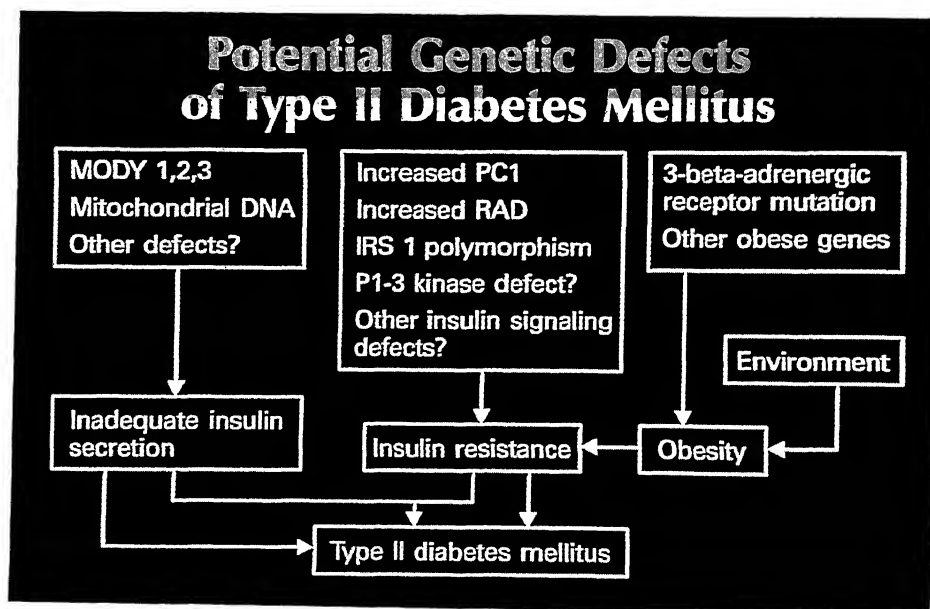


Fig.4 Nature–nurture interactions exemplified in the case of diabetes

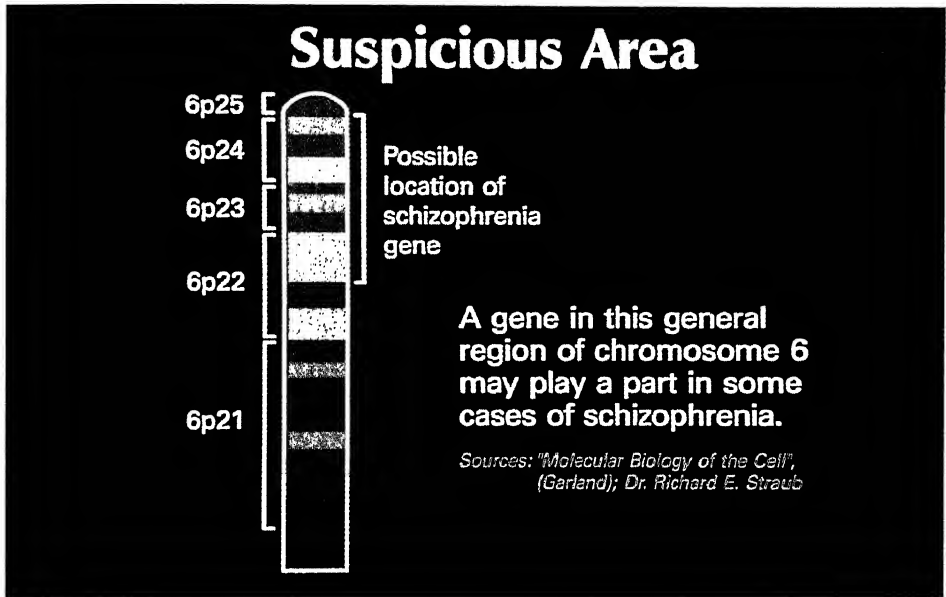
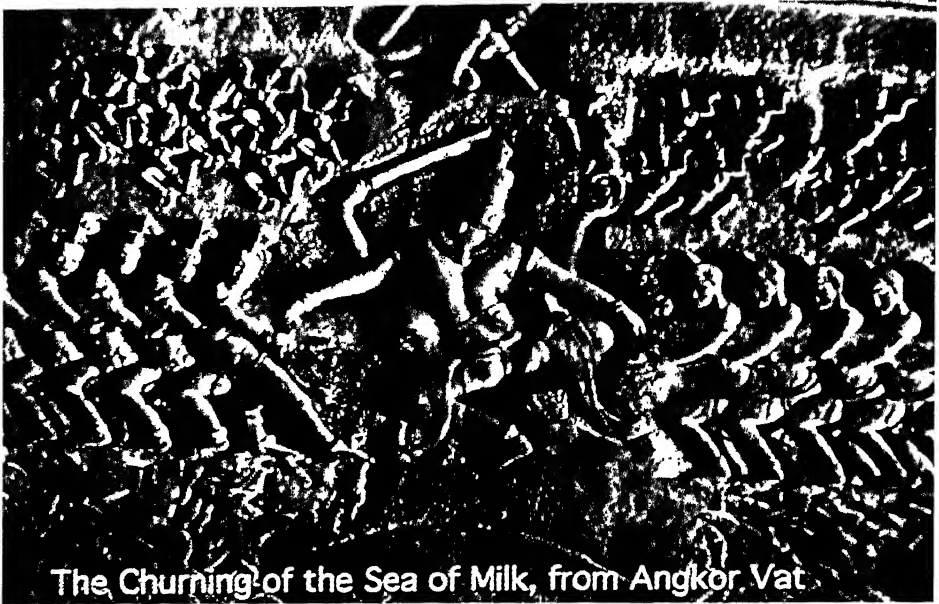


Fig.5 *Location of the genes for schizophrenia in the human chromosome number 6*



Fig.6 *The Angkor Vat temple of Cambodia*



The Churning of the Sea of Milk, from Angkor Vat

Fig.7 A temple frieze inside the Angkor Vat

"Human destiny is bound to remain a gamble, because at some unpredictable time and in some unforeseen manner, Nature will strike back."

Rene Dubos

(in *Mirage of Health*, 1959)

Fig.8

Over the years malaria has served as the paradigm in our understanding of natural selection in man. Malaria seems to have moulded the human genome during the course of human history more than any other disease, leaving behind its genetic footprints. The high mortality from *Plasmodium falciparum* malaria has drastically modified the human genome by the selection of genetic variants that reduce the risk of dying from malaria. Thalassaemia and sickle cell anaemia are examples of host-resistant genes that may modify the human host resistance to malaria. Malarial resistance genes might work through affecting: (i) the entry of parasites into red blood cells (RBCs); (ii) development of parasites within RBCs; or (iii) through the premature removal of infected RBCs.

The most recent findings of the Oxford Group led by Dr. Williams, published in *The Lancet*, raise exciting if tantalising questions in their studies with α -thalassaemia in the Polynesian island of Espiritu Santo in Vanuatu in relation to malaria. The hypothesis is that the young RBCs in thalassaemia with malarial infection act as a natural vaccine, hastening the acquisition of immunity; in a way malarial infection in α -thalassaemia seems to be acting as a live-attenuated vaccine.

When infection is a major cause of mortality, many genetic polymorphisms may be selected. These are of extreme importance to evaluate the human genome for factors that influence susceptibility or resistance to malaria and other infections. Not only haemoglobin but also red cell membranes, enzyme variants, Class 1 and Class 2 genes of the major histocompatibility complex (MHC), mutations in the tumour necrosis factor promoter region and non-MHC genes, such as intercellular adhesion molecules (ICAM), interferon and interleukin 1, 4, 10 and 12—all these seem to play a role in the interaction of infectious agents and human genome, influencing the final outcome.

HIV/AIDS

To take another recent example, the deletion of the *nef* gene from the genome of HIV 1 virus leading to resistance against HIV in the human host is again another fascinating aspect of interaction between genomes of invading organisms and the host human genome. These genetic variants should be viewed not as defects, but as polymorphic variants that serve the human genome well, in the context of providing selective advantage in the face of a life-threatening microbial invader.

I would like to close my opening remarks with a quotation from Rene Dubos (shown in Fig. 8).

β -Thalassemia in India—Molecular biology to community control of this blood disease

I. C. Verma and R. Saxena

Department of Genetic Medicine, Sir Ganga Ram Hospital, New Delhi

Abstract

β -Thalassemia is the most common single gene disorder in India with about 29 million carriers. It is a genetically inherited disorder of the blood, which is manifested as a severe form of anaemia, often fatal. About 7000 infants affected with homozygous β -thalassemia are born every year. Molecular lesions in 1200 β -thalassemia carriers from different states have been characterised so as to delineate the spectrum of mutations in India. This has enabled the prenatal diagnosis of β -thalassemia in about 450 pregnancies at risk, preventing the birth of 110 affected infants, and allowing the rest of the couples to have normal children, free from this debilitating disease.

For community control, after considering various options regarding whom to screen, it was decided to test pregnant women for their carrier status. Prenatal diagnosis in pregnancies where both husband and wife were carriers ensured the birth of normal children. In two pregnancies the foetus was found to be affected with homozygous β -thalassemia, and the parents opted for termination of pregnancy.

This paper outlines a possible model for the community control of β -thalassemia in India. The cost of avoiding the birth of affected infants is less than the cost incurred for the treatment of these children. It represents an example of progress from the understanding of the molecular biology to the community control of a severely burdensome disease in India.

Introduction

β -Thalassemia is the most common single gene disorder in India. Based on a number of studies conducted by the ICMR Task Force on Thalassemia [ICMR, 1993] as well as others [Choudhury and Verma, 1978; Modell and Petrou, 1983], the mean frequency of β -thalassemia carriers in India is about 3.3%, with a greater frequency of carriers in the northern, western and eastern parts of India (5.5% in Delhi, 2.6% in Mumbai and 10.2% in Calcutta). Given the current demographic data, this works out to about 29 million carriers in India.

About 7000 infants with homozygous β -thalassemia are born every year. This amounts to the birth of almost one infant with β -thalassemia every hour! The homozygous form

of the disease requires frequent blood transfusions and use of iron chelators (parenteral or oral). Blood for transfusion is in short supply; the transfusions themselves are hazardous because of possible transmission of hepatitis and AIDS viruses, while iron chelators are expensive. Bone marrow transplantation provides a definite cure but because of its enormous cost, is available to only a few patients.

Thus the only practical solution for the management of this disorder in India is community control to reduce the birth of affected children. No strategy for control is likely to be successful without the provision of prenatal diagnosis and selective abortion of the affected foetus. This was amply demonstrated by unsuccessful attempts at control before the era of prenatal diagnosis. If the number of affected children keeps on increasing, developing countries like India can never hope to have the resources to cope with and manage all affected children. Such a strategy for control has been successfully implemented in the West—in Cyprus, Sardinia and UK [WHO, 1983]. It has been a matter of debate whether a control programme for β -thalassemia can be implemented in India, because of its large size and the lack of funds.

The new tools of molecular biology have provided an easy and convenient means of prenatal diagnosis by analysis of DNA extracted from chorionic villus samples. However, before a simple and easy molecular method for accurate prenatal diagnosis can be used, it is necessary to know the mutations common in a community. This paper outlines how molecular characterisation of β -thalassemia mutations in people from different parts of India was carried out, extending the data of previous studies. The technology so developed was used for prenatal diagnosis in 450 pregnancies. Eventually, carrier testing was initiated among pregnant women, and selectively in the husbands of those women who were detected to be carriers of β -thalassemia, followed by prenatal diagnosis in the 'at risk' couples to avoid birth of affected children.

(a) Molecular mutations causing β -thalassemia

Over 150 different mutations that cause β -thalassemia have been reported from different parts of the world [Baysal and Carver, 1995]. Fortunately, in any population there are some common mutations and a few rare ones. In Asian Indians, five common and twelve rare mutations have been reported [Kazazian et al., 1984; Wong et al., 1986; Thein et al., 1988; Varawalla et al., 1991a, b; Jain et al., 1994].

Molecular mutations in about 1200 carriers of β -thalassemia from different parts of India have been analysed (migrants from Pakistan—690, Bengal—131, Punjab—99, Haryana—64, U.P.—71, Rajasthan—68, Bihar—39, Gujarat—34, other northern states—53, and southern states—31). This, combined with the studies by Parikh et al. (1990) in Mumbai, Varawalla et al. (1991a) in subjects from Mumbai, Delhi and South India, Venkatesan et al. (1992) in Chennai, Garewal et al. (1994) in subjects from Punjab and Mumbai, and Dastidar et al. (1994) in Bengal, provides excellent information about the distribution of mutations in different parts of India. The picture that emerges is as follows:

In our series [Verma et al., 1997a] 92% of subjects had one of the five most common mutations—IVSI-5 (G \rightarrow C), 619 bp deletion, IVSI-1 (G \rightarrow T), frameshift 8/9 (+G) and frameshift 41/42 (–CTTT). The frequency of these 5 mutations in the other studies was 88.1% [Thein et al., 1988], 89% [Parikh et al., 1990], 93.6% [Varawalla et al., 1991a] and 88% [Garewal et al., 1994].

The mutation IVSI-5 (G → C) was the predominant mutation in carriers from all over India, except among the migrants from Pakistan. This mutation has been the dominant Indian mutation in reports by Parikh et al. (1990) from Mumbai; Varawalla et al. (1991a) in subjects drawn from Mumbai, Punjab and Tamil Nadu; Venkatesan et al. (1992) from Tamil Nadu; Agarwal et al. (1994) from Lucknow in Uttar Pradesh; Garewal et al. (1994) from Mumbai and Punjab; and Dastidar et al. (1994) from Bengal.

Deletion of 619 bp was the most common mutation observed among migrants from Pakistan (about 30%). The frequency varies from 8 to 16% in states adjoining Pakistan while the frequency reduces to less than 5% in states away from Pakistan (e.g. Uttar Pradesh and Bengal), and none in southern states (Orissa, Karnataka, Andhra Pradesh and Tamil Nadu).

The mutation IVSI-1 (G → T) was observed with high frequency in migrants from Pakistan (about 25%), but with fairly low frequency in natives of Punjab and Rajasthan, and was not detected at all in carriers originating from West Bengal, Uttar Pradesh, Bihar and South India. Mutations frameshift 8/9 (+G) and frameshift 41/42 (−CTTT) are distributed in all regions of India with a frequency varying between 3 and 15%. Of the 'rare' mutations, codon 5 (−CT) and codons 47/48 (+ATCT) were found exclusively in migrants from Pakistan, while codon 88 (C → T) was reported only in subjects from Punjab, Haryana and Uttar Pradesh and not in Pakistani migrants, or Bengalis and South Indians. Mutations at codon 16 (−C), cap +1 (A → C), codon 15 (G → A), codon 30 (G → A) and codon 30 (G → C) were observed in carriers from all regions.

(b) Prenatal diagnosis of β -thalassemia

The immediate application of the knowledge of β -thalassemia mutations is to offer prenatal diagnostic service for families who have an affected child. This has been successfully done in India in a number of centres—Delhi, Mumbai, Lucknow, Chandigarh, Chennai, Hyderabad and Calcutta. The centres at Delhi and Mumbai have been the most active. Prenatal diagnosis has been carried out in about 450 pregnancies using the PCR-based amplification refractory mutation system (ARMS) employing allele specific primers [Saxena et al., 1997]. The ARMS technique was used as it is a simple, robust and nonisotopic technique [Old et al., 1990].

The causative mutations were first identified in the affected child and the parents. Each sample was initially screened for the five common mutations listed earlier. If no mutation was detected, the sample was analysed for the twelve rare mutations reported in Asian Indians (codon 16 (−C), cap +1 (A → C), codon 15 (G → A), codon 88 (C → T), codon 30 (G → A), codon 30 (G → C), codon 5 (−CT), frameshift 47/48 (+ATCT), IVS2 nucleotide 837 (G → T), nucleotide 1 (G → A), IVS1 nucleotide 110 (G → A) and codon 88 (+T)). Prenatal diagnosis was done by looking for the parental mutations in foetal DNA. Appropriate samples of DNA (positive and negative for the particular mutation) were amplified along with the foetal DNA. If the parental mutations were identical, the presence of the normal sequence at that site was examined by using appropriate allele specific primers. This allowed differentiation between homozygous and heterozygous states. In case the mutation was identified in one parent only, the presence or absence of this mutation in the CVS sample was determined.

Restriction fragment length polymorphism (RFLP) markers linked to β -globin gene were analysed to confirm the diagnosis in about 7% of cases, in whom either the parental mutations were unidentified or to confirm ARMS results especially in the presence of some of the rare mutations. The RFLPs studied were Hind II/ε, Hind III G_γ, Hind III/A_γ, Hind II/5' β, Hind II/3' β, Ava II/β, Hinf I/β, (Bam HI/β) and Xmn I/G_γ by previously described methods [Old and Ludlam, 1991; Varawalla et al., 1992].

In about 89% of carrier parents one of the five common Indian mutations was identified. Rare mutations were detected in about 7% parents, while the rest of the parents were negative for the 17 mutations identified in Asian Indians. In 94% of pregnancies, the mutations were recognized in both parents and a complete prenatal diagnosis was possible. Different mutations were present in about 55% of the couples. Identical mutations were identified in about 43% of the couples, which required the use of primers for the normal sequence at the site of the mutation for accurate prenatal diagnosis.

On molecular studies the expected number of fetuses were found to be normal, carriers or affected with β -thalassemia. In 3.9% of cases abortion ensued, mostly in the early part of the study. These could be either procedure-induced or spontaneous, since there were 3 cases which had an appointment for CVS at 10–12 weeks of gestation but reported a spontaneous abortion before the invasive procedure itself.

Based on the experience gained in the present study the following strategy is recommended for establishing prenatal diagnostic service in other centres. (i) The foetal sampling technique should be restricted to a limited number of obstetricians, who should gain experience by performing CVS in cases undergoing medical termination of pregnancy. (ii) Chorionic villi are the tissue of choice for obtaining foetal DNA. (iii) Expertise in separating chorionic villi tissue from decidual (maternal) tissue must be acquired. (iv) One of the PCR-based non-isotopic methods should be used as the laboratory technique—e.g. reverse dot blot, dot blot or 'ARMS'. (v) Samples positive and negative for the mutation being analysed must be tested at the same time using the same reagents and chemicals, as well as a sample with no DNA template. (vi) If the diagnosis is based only on the presence of the maternal mutation in the foetal DNA, maternal contamination should be excluded by study of polymorphic genes like apoB. (vii) If parental mutation(s) remain unidentified, diagnosis should be sought using linkage studies, or DGGE or SSCP analysis.

(c) Community control of β -thalassemia

The components of a strategy for community control have been well enunciated by WHO (1983), and also outlined by the authors [Verma et al., 1992; Varawalla, 1992]. Essentially it requires proper management of children having thalassemia major, carrier screening in the population and prevention of births of affected children through prenatal diagnosis. These have to be preceded by community education and information. For the success of such a programme political will, public backing, manpower trained in the appropriate techniques, and adequate financial support are essential.

Carrying out prenatal diagnosis in future pregnancies of affected couples helps the concerned families but does not reduce the burden of the disease in the community, because all cases of first affected child are not prevented by this approach. For this purpose, some type of prospective screening for carriers is essential.

Regarding screening for carrier status, a number of options to identify a target population are available—high school or college students, after marriage and during pregnancy. It is logistically convenient and easy to screen pregnant women. Moreover, during pregnancy, women are well motivated and readily agree to being tested. That is why this group was chosen for screening to gain experience in trying to develop a community control programme. However many women are screened in an advanced stage of pregnancy and in such cases, prenatal diagnosis may not be possible due to advanced gestation, as abortion of an affected foetus is not legally permissible beyond 20 weeks of gestation in India. This is the drawback in targeting pregnant women for screening.

The ideal strategy, of course, would be to screen couples after marriage but before pregnancy to identify couples at risk (i.e. both partners are carriers). A lot of effort will be required in educating the community members to come forward to be screened after marriage but before pregnancy. In the current social milieu the authors do not recommend screening before marriage. In India relatives of the affected families may be targetted for screening, as was done by Cao and co-workers (1989) in Sardinia (called by them as inductive screening). This strategy has been successful in preventing the birth of affected infants by almost 60%.

Nevertheless, screening of 2300 pregnant women in a district hospital yielded a carrier rate for β -thalassemia of 2.7%. Only about two-thirds of the husbands of carrier women came forward to be tested, and of these, about 15% turned out to be carriers [Verma et al., 1997b]. This was an unexpectedly high figure, and is explained on the basis of endogamous marriages in India. Prenatal diagnosis in these couples led to the prevention of the birth of two affected infants. The cost of treatment of the two affected children for a period of 10 years would roughly be Rs. 20 lakhs, not considering the effort and cost of almost innumerable blood transfusions over this period, and the attendant morbidity, and the time and effort spent by the parents in obtaining medical care for the children. The cost of screening 2300 pregnant women, their husbands and of prenatal diagnosis which was done in the 'at risk' couples would not exceed Rs.15 lakhs for all expenses (staff and equipment included). This makes a strong case on economic considerations to go in for community control of β -thalassemia in regions of high prevalence in India.

The ICMR has funded a five-centre study to evaluate the usefulness and to standardise the technology for antenatal screening of pregnant women, with the aim to prevent the birth of affected children. Concurrently with the help of Thalasseemics India—a parents' organisation for β -thalassemia—thalassemia awareness and screening campaigns are being conducted in schools and colleges in Delhi. This will pave the way for a true community control programme in Delhi.

Acknowledgements

The authors wish to thank the dedicated members of the team who have helped in the successful implementation of this project, especially Dr. Pawan K. Jain, former Senior Research Officer, Genome Project, Dept. of Biotechnology; Arti Gulati, Research Officer, ICMR Project; and Elizabeth Thomas, Laboratory Technician in the DBT Project.

The authors also wish to thank the Indian Council of Medical Research and the Dept. of Biotechnology, Government of India, for financial support for the research work reported herein, and the All India Institute of Medical Sciences where most of this work was carried out.

References

1. Agarwal, S., Naveed, M., Gupta, U.R., Kishore, P. and Agarwal, S.S. (1994). Characterization of β -thalassemia families seen at Lucknow. *Indian J. Med. Res.* **100**, 106–110.
2. Baysal, F. and Carver, M.F.J. (1995). The β - and δ -Repository. 8th edition. *Haemoglobin*. **19**, 213–236.
3. Cao, A., Rosatelli, C., Galanello, R., Monni, G., Olla, G., Cossu, P. and Ristadi, M.S. (1989). The prevention of thalassemia in Sardinia. *Clin. Genet.* **36**, 277–285.
4. Choudhury, V.P. and Verma, I.C. (1978). Thalassemia in India: Problems and future prospects. In *Medical Genetics in India*. (Ed. I.C. Verma). Auroma Enterprises, Pondicherry. **II**, 245–254.
5. Dastidar, D.G., Dutta, R.N., Gupta, P. and Old, J.M. (1994). Detection of β -thalassemia in eastern Indian population by polymerase chain reaction. *Indian J. Med. Res.* **100**, 111–114.
6. Garewal, G., Fearon, C.W., Warren, T.C., Marwah, N., Marwah, R.K., Mahadik, C. and Kazazian, H.H. Jr. (1994). The molecular basis of β -thalassemia in Punjabi and Maharashtrian Indians includes a multilocus etiology involving triplicated α -globin loci. *Br. J. Haematol.* **86**, 372–376.
7. ICMR Collaborative Study on Thalassemia. An ICMR task force study. (1993).
8. Jain, P.K., Dozy, A.M., Verma, I.C. and Chehab, F.F. (1994). A new frameshift mutation, insertion of ATCT, at codon 48 in the β -globin gene causes β -thalassemia in an Indian proband. *Hum. Mutation*. **3**, 397–398.
9. Kazazian, H.H. Jr., Orkin, S.M., Antonarakis, S.E., Sexton, J.P., Boehm, C.D., Goff, S.C. and Waber, P.G. (1984). Molecular characterization of seven β -thalassemia mutations in Asian Indians. *EMBO Journal*. **3**, 593–596.
10. Modell, C.B. and Petrou, M. (1983). The problem of haemoglobinopathies in India. *Indian J. Haematol.* **1**, 5.
11. Old, J.M., Varawalla, N.Y. and Weatherall, D.J. (1990). Rapid detection and prenatal diagnosis of β -thalassemia: Studies in Indian and Cypriot populations in the U.K. *Lancet*. **336**, 834–837.
12. Old, J.M. and Ludlam, C.A. (1991). Antenatal diagnosis. In: *Bailliere's Clinical Haematology*. **4**, 391–428.
13. Parikh, P., Cotton, M., Boehm, C.D. and Kazazian, H.H. (1990). Ethnic distribution of β -thalassemia in Indian subcontinent. *Lancet*. **336**, 1006.

14. Saxena, R., Jain, P.K., Thomas, E. and Verma, I.C. (1997). Prenatal diagnosis of β -thalassemia: Experience in a developing country. *Prenat. Diagn.* (in press).
15. Thein, S.L., Hesketh, C., Wallace, R.B. and Weatherall, D.J. (1988). The molecular basis of thalassemia major and thalassemia intermedia in Asian Indians: Application to prenatal diagnosis. *Br. J. Haematol.* **70**, 225–231.
16. Varawalla, N.Y., Old, J.M., Sarkar, R., Venkatesan, R. and Weatherall, D.J. (1991a). The spectrum of β -thalassemia mutations on the Indian subcontinent: The basis for prenatal diagnosis. *Br. J. Haematol.* **78**, 242–247.
17. Varawalla, N.Y., Old, J.M. and Weatherall, D.J. (1991b). Rare β -thalassemia mutations in Asian Indians. *Br. J. Haematol.* **79**, 640–644.
18. Varawalla, N.Y. (1992). Prenatal diagnosis and control strategies for β -thalassemia on the Indian subcontinent. *Natl. Med. J. India.* **5**, 157–161.
19. Venkatesan, R., Sarkar, R. and Old, J.M. (1992). β -thalassemia mutations and their linkage to β -haplotypes in Tamil Nadu in Southern India. *Clin. Genet.* **42**, 251–256.
20. Verma, I.C., Choudhury, V.P. and Jain, P.K. (1992). Prevention of thalassemia—Necessity in India. *Indian J. Pediatr.* **59**, 649–654.
21. Verma, I.C., Saxena, S., Thomas, E. and Jain P.K. (1997a). Regional distribution of β -thalassemia in India. *Hum. Genet.* (In press).
22. Verma, I.C., Maheshwari, M. and Gulati, A. (1997b). *Community control of β -thalassemia in India—A pilot study.* (Under publication).
23. Wong, C., Antonarakis, S.E., Goff, S.C., Orkin, S.H., Boehm, C.D. and Kazazian, H.H. (1986). On the origin and spread of β -thalassemia: Recurrent observation of four mutations in different ethnic groups. *Proc. Natl. Acad. Sci. USA.* **83**, 6529–6532.
24. World Health Organisation. (1983). Report on the community control of hereditary anemias: Memorandum from a WHO meeting. *Bull. WHO.* **61**, 63–80.

3

Consanguinity—A common human heritage? The effects on the health and well-being of Indian populations

N. Appaji Rao, H.S. Savithri, A. Radha Rama Devi
Department of Biochemistry,
Indian Institute of Science, Bangalore

A.H. Bittles
Centre for Human Genetics,
Edith Cowan University, Perth,
Western Australia

Abstract

The topic of inbreeding in human populations has long fascinated geneticists, sociologists and philosophers. Among the populations throughout North and sub-Saharan Africa, the Middle East, and Central and South Asia, marriages between couples related as second cousins or closer, still account for 20% to over 50% of all unions. By comparison, in Western societies generally negative views on close kin marriages have predominated, due mainly to historical, social and religious prejudices. As a result, unions of this type are rare in the West.

It can be predicted that autosomal recessive traits will be more common in the progeny of consanguineously related parents, since they have a greater chance of inheriting identical copies of a mutant gene or genes from a common ancestor. However, in communities with a long and unbroken history of consanguineous unions, it has been hypothesised that deleterious genes would have been substantially eliminated from the gene pool. In addition, there is the suggestion that factors such as changing family structure and urbanisation would result in a large decrease in close kin marriages.

We have attempted to assess the effect of consanguinity on the prevalence of genetic disorders, and more generally on reproductive behaviour and postnatal mortality. Between 1980 and 1989, we examined some 107,500 newborn children in Bangalore and Mysore as part of a systematic neonatal screening programme. In addition, mentally retarded and sick children referred to us with suspected genetic disorders were investigated. Contrary to earlier prediction, consanguinity was still widely prevalent among Hindus (33.5%) with a mean inbreeding coefficient (F) of 0.0333, Muslims (23.7%) with $F = 0.0160$, and Christians (18.6%) with an F value of 0.0173. The comparative value for industrialised Western populations is less than 1% consanguineous marriage, with an approximate F value of 0.0003.

Surprisingly, the prevalence of inherited amino acid disorders in Karnataka was of the same magnitude as in outbred populations, and a simple statistical analysis of the data on numbers of liveborn and living children by consanguinity class failed to reveal a significant consanguinity effect. Multivariate analysis did indicate that excess mortality was associated

with consanguinity in a minority of families, and a separate analysis of data collected on sick children also revealed the adverse influence of consanguinity. Paradoxically, among Vysas who do not practise consanguinity, the incidence of the autosomal disorder pseudocholinesterase deficiency was high.

It is apparent that in many earlier studies into the effects of consanguinity on fertility, and prenatal and postnatal mortality, adequate allowance for socio-demographic variables was not made. Our studies have emphasised the social, cultural and economic benefits of consanguineous marriage in regions such as South India and, in assessing the needs of the minority of consanguineous families with genetic disorders, due attention should be given to these benefits. At the same time, there is an urgent need for the rapid development of appropriate medical care and genetic counselling for consanguineous and non-consanguineous couples alike.

Introduction

In Western countries, it is widely believed that inbreeding is confined to poor, isolated and backward communities, whose inhabitants suffer from diverse physical disorders and frequently exhibit symptoms of mental subnormality. This myth is perpetuated in large measure due to historical, religious and social prejudices, epitomised by the ban on marriages among close relatives imposed by the Latin Church in the early days of its development in Europe. At one stage the Church ban extended to marriages up to and including third cousins, but the ruling was relaxed in the present century and dispensation is now required only for the solemnisation of first cousin marriages [Goody, 1990; Ottenheimer, 1990; Bittles, 1994]. In the United States of America, eight states treat marriages between first cousins as a criminal offence, and in 31 other states they are a civil offence [Brett, 1984]. Uncle–niece unions are generally regarded as invalid, and in India, the Hindu Code Bill of 1984 also prohibits such marriages, except where permitted by prevailing social customs as in the four southern states—Andhra Pradesh, Karnataka, Kerala and Tamil Nadu.

The fascination of biologists and social scientists with the effects of inbreeding in human populations is due to the observation that, in general, the offspring of consanguineous unions exhibit a higher level of early morbidity and mortality. At first cousin level it has been estimated that cumulative, consanguinity-associated mortality up to early adulthood is, on an average, 4.4% higher than in non-consanguineous progeny [Bittles and Neel, 1994]. In definitional terms, two individuals are said to be consanguineous if they have at least one ancestor in common, and the progeny of consanguineous parents are often described as inbred. Where an individual has identical copies of a gene/allele at a particular locus, he/she is said to be homozygous with respect to that locus. It is possible to differentiate between homozygosity due to descent from a common ancestor (autozygosity) and where no common ancestor exists (allozygosity). The coefficient of inbreeding (F) is a measure of the probability that at a given locus an individual has inherited two copies of a gene that are identical by descent. In the most commonly observed forms of consanguineous marriage, the coefficients of inbreeding are—uncle–niece: $F = 0.125$, first cousin: $F = 0.0625$ and second cousin: $F = 0.0156$.

The mean inbreeding coefficient (F or α) of a population is given by $F = \sum p_i F_i$ where Σ is the sum of the proportion of couples (p_i) in each specific consanguinity class (F_i). In communities with a long and continuous history of consanguineous marriage, the cumulative F value is given by $\Sigma(1/2)^n(1 + F_A)$, where n denotes the number of individuals in the path connecting the parents of the individual, and the term $(1 + F_A)$ is the contribution of the ancestors' own inbreeding coefficient.

We discuss here the prevalence of consanguinity in India and other parts of the world, its effects on the incidence of genetic disorders, on mortality and morbidity, and the inter-relationships between consanguineous unions and social, economic and demographic factors.

Genetic consequences of inbreeding

The increased prevalence of genetic disorders which may be found in the progeny of consanguineous marriages is due to the expression of rare, recessive genes inherited from a common ancestor. When outbreeding is the norm, the presence of close kin marriage is often taken as evidence that, in some way, consanguinity has contributed to a disorder which may be genetic in origin. Conversely, almost three decades ago it was suggested by Dr. L.D. Sanghvi that continuous inbreeding could have resulted in the elimination of deleterious genes from the South Indian gene pool, because of the pre-reproductive deaths of individuals who were homozygous for a lethal, recessive gene [Sanghvi, 1966]. In our studies, and acting on the assumption that consanguineous marriage had long been preferred in South India, the questions we wished to address were whether this would have led to:

- (i) an increased incidence of genetic disorders, or alternatively,
- (ii) the elimination of deleterious genes.

A previous study conducted on children reporting to one of the clinics at the National Institute of Mental Health and Neurosciences (NIMHANS), Bangalore showed that of the 1,280 patients examined, there were 14 cases of phenylketonuria, 5 of maple syrup urine, 4 of Hartnups disease, 2 of homocystinuria and 3 of mucopolysaccharidosis [Sridhara Rama Rao, 1995; Sridhara Rama Rao et al., 1977]. These observations suggested that, in spite of the presumed long tradition of inbreeding in Karnataka, autosomal recessive disorders were still present in the population. Therefore, estimates of the incidence of genetic disorders or their relationship to consanguinity cannot meaningfully be drawn from the results obtained with this highly preselected group of patients. For this purpose, it was necessary to examine a representative sample of the general population.

Neonatal screening for the detection of amino acidopathies—the Karnataka study

An important aspect of a number of amino acid disorders is that, to a large degree, their severity can be ameliorated by the early introduction of a specially formulated diet. For

such treatment to be optimally effective, it has to begin within a few weeks of birth. A presymptomatic screen of neonates in Bangalore and Mysore started in 1980 and, after overcoming initial organisational problems, it continued until 1989 when the goal of more than 100,000 newborns tested was passed [Appaji Rao et al., 1988; Appaji Rao, 1991]. The programme included 50 hospitals and nursing homes in Bangalore and Mysore. Besides collecting three drops of blood by toe prick from 3–4 day old infants after they had taken at least 3 feeds, trained staff interviewed the mothers to obtain information on her relatedness to her spouse, religion, age, the sex of the baby, the number of liveborn and living children and on singleton/multiple births [Radha Rama Devi et al., 1981]. Informed consent was obtained from mothers after the features of the programme had been explained to them, and permission also was granted by the superintendents of the various hospitals and nursing homes. The information was first entered manually into registers, and then encoded and stored on computer. A blood spot (0.6 cm diameter) was excised and eluted overnight into 50 μ l of 50% ethanol. An aliquot (2–5 μ l) of this extract was then subjected to thin layer chromatography using a butanol:acetone:acetic acid:water solvent system, and individual amino acids were detected by reaction with ninhydrin [Ireland and Reed, 1972]. By this method, 13 to 17 discreet amino acid bands were routinely identified in the neonatal samples.

The results of our study showed that consanguineous marriages were still strongly preferred in Karnataka. Table 1 shows that of the approximately 107,500 infants examined, 62.3% were born to non-consanguineous couples, 17.1% to an uncle–niece union, 11.4% to first cousins and 1.8% to second cousins and the mean coefficient of inbreeding in the population was $F = 0.0298$. In order to place the study in perspective, it may be helpful to briefly discuss the global prevalence of inbreeding. As previously noted, it has been widely assumed in Western societies that consanguinity was confined to socially or geographically isolated, minority communities. Further, that the prevalence of consanguineous unions had significantly decreased in recent generations. In fact, consanguineous marriage is still strongly preferred in many parts of the world, as evidenced in nearly 100 studies published between 1957 and 1994 [Bittles, 1990 and 1994], with sample sizes ranging from 252 to 843,941. For example, in North and sub-Saharan Africa, the Middle East, Central and South Asia, with a combined population in excess of 750 million, consanguineous marriages currently account for 20% to over 50% of all unions. These data on the global distribution of consanguineous unions should be regarded as conservative as, for example, no substantial results are yet available for the populations of China or Indonesia where there are indications that consanguinity is still practised. A comparison of our data with studies in Pakistan may be interesting. In a survey of 9,520 marriages in the Pakistani province of Punjab [Bittles, Grant and Shami, 1993], 50.4% were contracted between second cousins or closer with a mean F value of 0.0280. In addition, 33.9% marriages were *bradari* (literally brotherhood) relationships with both partners belonging to the same social/occupational group [Shami, Grant and Bittles, 1994]. This situation contrasts sharply with the Hindu populations of North India where, following the dictum of Manu, consanguineous marriages are strenuously avoided [Kapadia, 1958; Roychoudhury, 1976], and Western countries such

as the UK [Coleman, 1980] and USA [Lebel, 1983], in which consanguineous unions account for less than 1% of all marriages.

Table 1 *Consanguinity profiles of parents of neonates screened for amino acidemia in Bangalore and Mysore, Karnataka from January 1, 1980 to December 31, 1989*

Class	F	Number	Percentage
Uncle-niece	0.125	19,160	17.1
First cousin	0.0625	12,578	11.4
Second cousin	0.0156	1,995	1.8
Beyond second cousin	< 0.0156	4,632	4.1
Non-consanguineous	-	69,153	62.3
Unknown	-	3,768	3.3

From Table 2 it can be seen that in the neonatal screening programme, 45 cases of single amino acid disorders were detected and 70 infants showed a general amino acidemia. Repeat blood sampling and follow-up were possible in 57% of cases. Although some 107,500 neonates were analysed, an accurate estimate of the incidence of inherited amino acid disorders in the population could not be derived because of the notable subdivision of the study sample by religion, language and caste. In addition, it was not possible to test all children born in Bangalore and Mysore on sequential basis during the study period, as the sampling was conducted between the second and fifth day of life and there may have been mis-diagnosis in a small number of positive subjects who had been poor feeders. This situation could have been further exacerbated by the fact that, in a small number of cases, mothers had followed the local tradition of feeding the newborn with glucose solution, despite strong discouragement from the medical and nursing staff [Appaji Rao et al., 1988]. The inbreeding coefficient for infants with single amino acidemias was $F = 0.0336$, compared to values of 0.0350 and 0.0298 for generalised amino acidemias and the total newborn population respectively. At follow-up, some of the cases showed normal amino acid profiles—in particular, in neonates with tyrosinaemia—where foetal immaturity appeared to be a significant contributory factor to the initial positive finding [Appaji Rao et al., 1988]. The earlier predicted high rate for the occurrence of phenylketonuria in Karnataka based on the study of mental retardates [Sridhara Rama Rao, 1995; Sridhara Rama Rao et al., 1977] was not supported by this prospective study on the general newborn population.

Table 2 *Amino acidemias detected during neonate screening in Karnataka (1980–89)*

Disorder	Number	Prevalence
Hyperphenylalaninaemia	6	1/18,726
Tyrosinaemia	18	1/6,242
Glycinaemia	7	1/26,052
Branched chain amino acidemia	11	1/10,215
Histidinaemia	3	1/37,454
General amino acidemia	70	1/1,605

When we examined a cohort of 404 sick children referred by local clinicians with suspected genetic disorders, a different situation was encountered, with a variety of genetic disorders detected (Table 3). The thirtyfive abnormalities diagnosed ranged from amino acid disorders such as phenylketonuria, tyrosinaemia, histidinaemia and branched chain amino acidemia, to carbohydrate, purine, pyrimidine, lysosomal, connective tissue and transport disorders, and chromosomal and polygenic defects [Radha Rama Devi et al., 1987]. The role of inbreeding in the aetiology of these disorders was apparent by comparing the F value of the entire study group (0.0414) with that of children with single gene defects (0.0513). When only autosomal recessive disorders were considered, the association became even more striking, as the mean F value increased, to 0.0625. This particular study therefore confirmed that a wide range of genetic disorders were still present in the population of Karnataka and continued inbreeding had not resulted in their elimination.

Table 3 *Genetic disorders detected in sick children*

Type	Number	Percentage
Autosomal recessive	11	2.7
Autosomal dominant	24	5.9
X-linked	5	1.2
Chromosomal	7	1.7
Polygenic	12	4.0
Uncertain	4	1.0
Total cases	404	100

In addition to collecting blood samples from newborn infants for the detection of genetic disorders, mothers were interviewed to obtain information on consanguinity, their liveborn and living children, mother's age, religion and the prevalence of twinning, with data on the baby's age, sex and the name of the hospital/nursing home also recorded. Although the poorest section of society and the wealthiest families were under-represented, the sample did reasonably reflect the overall socio-economic spectrum of the residents of Bangalore and Mysore.

During the course of the study, a preliminary analysis of the data of the population of Karnataka ($n = 65,492$) was carried out [Bittles et al., 1987]. It can be seen from Table 4 that the mean numbers of liveborn and living children were lower in non-consanguineous couples compared to the consanguineous group as a whole. A χ^2 test showed no statistically significant trend in terms of either liveborn or living children with increasing inbreeding, although an analysis of variance conducted after arcsin transformation of the mortality data from each consanguinity class and by religion strongly suggested that there was a consanguinity-related increase in deaths in the population. However, against the high level of background mortality due to infectious and nutritional diseases, this increase was not statistically significant.

Table 4 *Mean and variance of liveborn and living children by consanguinity class*

Class	Liveborn			Living children		
	Number	Mean	Variance	Number	Mean	Variance
Uncle–niece	44,417	2.28	± 0.61	42,537	2.18	± 0.53
First cousin	29,721	2.35	± 0.66	28,450	2.25	± 0.56
Second cousin	4,791	2.32	± 0.59	4,510	2.24	± 0.53
Beyond second cousin	22,281	2.33	± 0.62	20,903	2.26	± 0.54
Non-consanguineous	1,53,797	2.20	± 0.41	1,47,893	2.12	± 0.38

In order to examine these issues in greater detail, a more sophisticated multivariate analysis of the data was subsequently conducted on the outcomes of 107,518 marriages [Bittles et al., 1991]. The aims of the analysis were to determine the relationships between consanguinity, mother's age at first birth, mean number of children born, the odds of a child dying versus no death and, among mothers who had lost more than one child, the odds of two or more children dying versus one death. The interaction of these parameters with religion and hospitals was additionally examined. The results indicated that mean maternal age at first livebirth was lowest in the Muslim community and highest among Christians. On average, Muslim women reported the largest family sizes which were positively associated with consanguinity [Bittles et al., 1991; Bittles, Shami and Appaji Rao, 1993]. It was also apparent that the loss of one child or more showed a positive association with consanguinity, which is consistent with a genetic aetiology. Overall, 7.9% of the families had lost one child or more, and 3.0% had lost two children or more. Our data indicated that mothers in the age group 15–19 years had the highest chance of experiencing the death of an infant, and those aged 20–34 the least. In the absence of information on cause of death it is difficult to identify the precise contribution of a genetic component to mortality; however, it is appropriate to recall that a wide variety of genetic disorders had earlier been diagnosed in the community [Radha Rama Devi et al., 1987].

Another complicating factor in assessing the data was the paucity of information on socio-economic status, although the hospital type gave some indication of this factor since Government hospitals were almost exclusively the choice of the poorest families, whereas the richer communities preferred private nursing homes. Interestingly, and as might have been expected, in general terms, women delivering in private nursing homes reported the highest age at first birth, the fewest liveborns and the lowest mortality. These findings emphasise the need for reliable information on socio-economic status when assessing the effect of consanguinity on fertility and mortality. Where such data are not available, there is a real danger that erroneous conclusions may be drawn and, since the highest rates of consanguinity are usually found among the poorest and least educated communities, the adverse effects associated with consanguinity could be exaggerated [Bittles et al., 1991; Bittles, 1994].

Pseudocholinesterase deficiency among Vysas

As part of our studies, an investigation was conducted into the single gene defect pseudocholinesterase deficiency, since it had been reported that many members of the Vysa community suffered from this disorder [Rao and Gopalan, 1979]. The deficiency leads to scoline apnoea, i.e., scoline administered prior to anaesthesia cannot rapidly be degraded as in normal individuals, leading to prolonged muscular paralysis and a requirement for ventilatory support if death is to be averted. The mutant genotype may be characterised by decreased pseudocholinesterase activity and/or altered inhibition constants for dibucaine and fluoride. Pseudocholinesterase activity was determined among Vysas resident in the states of Karnataka and Andhra Pradesh and inhibitor constants evaluated for dibucaine and fluoride [Rao and Gopalan, 1979; Whittaker, 1977]. Comparison between the control population and among Vysa subjects revealed that the mean pseudocholinesterase activity in the Vysas is reduced substantially. In 4 of the 110 Vysas tested, pseudocholinesterase activity was barely detectable. However, the dibucaine and fluoride numbers were similar in both groups, suggesting that the mutation was of the silent variety.

An initially surprising aspect of this study was the near-absence of consanguinity in the Vysas, with only one consanguineously related couple reported (0.9%) compared to 33.5% of all marriages in the general population. What this demonstrates is that, even in the absence of consanguinity, an autosomal recessive defect can increase to high frequency in a strictly endogamous community due to the action of founder effect and genetic drift. From a more general perspective, the finding reinforces the need for caution when assessing the data on recessive disorders in populations where consanguinity is generally favoured.

Summary and Conclusion

Inbreeding in humans can variously occur as a rare event in a large population where outbreeding is the norm, in population isolates of restricted size when mate choice is restricted, and in major populations where consanguinity is preferential for social, cultural or religious reasons [Bittles, 1980, 1994]. The problems resulting from inadequate control for socio-economic status when assessing the biological effects of consanguinity were illustrated in studies in Japan [Neel and Schull, 1962; Schull and Neel, 1972], and the complex inter-relationships between consanguinity and demographic variables, such as maternal education and birth interval, have recently been demonstrated as part of a national Demographic and Health Survey in Pakistan [Grant and Bittles, 1997].

Consanguineous marriage is often the first choice, or in some instances may be mandatory, for a significant percentage of populations in Africa and Asia. It has been predicted that, with the break-up of joint family systems, urbanisation, and large-scale population movement, there would be a major decrease in the prevalence of marriage among close relatives. Our studies in Karnataka indicate that, to date, these predictions have not proved to be valid [Bittles, Coble and Appaji Rao, 1993]. Likewise, in Pakistan [Grant and Bittles, 1997; Bittles, 1990] and among Pakistani migrants in the UK

[Bundey and Alam, 1993; Modell, 1991], there is no evidence of a decline in the popularity of consanguineous unions. In fact, with increasing emphasis on fundamentalist religious doctrines and high population growth in many populations which traditionally favour consanguinity, it seems probable that in the near future there will actually be an increase in the global numbers and proportions of consanguineous unions.

With improving standards of health in India and many other Asian countries, due to factors such as improved sanitation, better nutrition and vaccination for childhood infectious diseases, infant and childhood mortality is steadily declining. It can be predicted that this trend will be accompanied by an epidemiological transition in which genetic disorders will increasingly contribute to early morbidity and mortality. Although the Karnataka study has emphasised that increased consanguinity-associated mortality occurs in only a minority of families, it is important that their specific health-needs be met. Therefore further in-depth studies into all aspects of consanguinity should be urgently undertaken, for example, into topics such as glucose 6-phosphate dehydrogenase deficiency [Rama Devi et al., 1994a, b], with unique enzyme variants reported and low rates of enzyme activity in South Indian females as well as males, and the effects of long-term inbreeding on the structure of the genome. However, to ensure that the information thus gained is efficiently translated into beneficial action within the community, education programmes need to be introduced with, as a high priority, the training of genetic counsellors conversant with local social customs and preferences.

References

1. Appaji Rao, N., Radha Rama Devi, A., Savithri, H.S., Venkat Rao, S. and Bittles, A.H. (1988). Neonatal screening for amino acidurias in Karnataka, South India. *Clinical Genetics*. **34**, 60–63.
2. Appaji Rao, N. (1991). Genetic consequences of inbreeding in large populations. *Proceedings of the Indian National Science Academy*. **B57**, 361–368.
3. Bittles, A.H., Coble, J.M. and Appaji Rao, N. (1993). Trends in consanguineous marriages in Karnataka, South India. *Journal of Biosocial Science*. **25**, 111–116.
4. Bittles, A.H., Grant, J.C. and Shami, S.A. (1993). Consanguinity as a determinant of reproductive behaviour and mortality in Pakistan. *International Journal of Epidemiology*. **22**, 463–467.
5. Bittles, A.H., Mason, W.M., Greene, J. and Appaji Rao, N. (1991). Reproductive behavior and health in consanguineous marriages. *Science*. **252**, 789–794.
6. Bittles, A.H., Radha Rama Devi, A., Savithri, H.S., Sridhar, R. and Appaji Rao, N. (1987). Consanguineous marriage and postnatal mortality in Karnataka, South India. *Man (NS)*. **22**, 736–745.
7. Bittles, A.H., Shami, S.A. and Appaji Rao, N. (1993). Consanguineous marriage in southern Asia: incidence, causes and effects. In *Minority Populations: Genetics, Demography and Health*. Macmillan, London. 102–118.
8. Bittles, A.H. and Neel, J.V. (1994). The costs of human inbreeding and their implications for variations at the DNA level. *Nature Genetics*. **8**, 117–121.
9. Bittles, A.H. (1980). Inbreeding in human populations. *Biochemical Reviews*. Golden Jubilee. **50**, 108–117.

10. Bittles, A.H. (1994). The role and significance of consanguinity as a demographic variable. *Population and Development Review*. **20**, 561–583.
11. Bittles, A.H. (1990). Consanguineous marriage: Current global incidence and its relevance to demographic research. Research Report. Population Studies Center, University of Michigan. 90–186.
12. Brett, L.S. (1984). Incest statutes and the fundamental right of marriage: Is Oedipus free to marry? *Family Law Quarterly*. **18**, 257–309.
13. Bunday, S. and Alam, H. (1993). A five-year prospective study of the health of children in different ethnic groups, with particular reference to the effect of inbreeding. *European Journal of Human Genetics*. **1**, 206–219.
14. Coleman, D. (1980). A note on the frequency of consanguineous marriages in Reading, England, in 1972/1973. *Human Heredity*. **30**, 278–285.
15. Goody, J. (1990). *The development of the family and marriage in Europe*. Cambridge University Press, Cambridge.
16. Grant, J.C. and Bittles, A.H. (1997). The comparative role of consanguinity in infant and child mortality in Pakistan. *Annals of Human Genetics*. **61**, 143–149.
17. Ireland, J.T. and Reed, R.A. (1972). A thin layer chromatography method for use in neonatal screening to detect excess amino acidemia. *Annals of Clinical Chemistry*. **9**, 129–132.
18. Kapadia, K.M. (1958). *Marriage and the Family in India*. Oxford University Press, Calcutta. 2nd. edition. 117–137.
19. Lebel, R.R. (1983). Consanguinity studies in Wisconsin. I. Secular trends in consanguineous marriages, 1843–1981. *American Journal of Medical Genetics*. **15**, 543–560.
20. Modell, B. (1991). Social and genetic implications of customary consanguineous marriage among British Pakistanis. *Journal of Medical Genetics*. **28**, 720–723.
21. Neel, J.V. and Schull, W.J. (1962). The effect of inbreeding on mortality and morbidity in two Japanese cities. *Proceedings of the National Academy of Sciences (U.S.A.)*. **48**, 573–582.
22. Ottenheimer, M. (1990). Lewis Henry Morgan and the prohibition of cousin marriages in the United States. *Journal of Family History*. **15**, 325–334.
23. Radha Rama Devi, A., Appaji Rao, N. and Bittles, A.H. (1981). Consanguinity, fecundity and post-natal mortality in Karnataka, South India. *Annals of Human Biology*. **8**, 469–472.
24. Radha Rama Devi, A., Appaji Rao, N. and Bittles, A.H. (1987). Inbreeding and the incidence of childhood genetic disorders in Karnataka, South India. *Journal of Medical Genetics*. **24**, 362–365.
25. Ramadevi, R., Savithri, H.S., Bittles, A.H. and Appaji Rao, N. (1994). Characterization of a variant glucose 6-phosphate dehydrogenase from the South Indian population. *Indian Journal of Biochemistry and Biophysics*. **31**, 361–365.
26. Ramadevi, R., Savithri, H.S., Radha Rama Devi, A., Bittles, A.H. and Appaji Rao, N. (1994). An unusual distribution of glucose 6-phosphate dehydrogenase deficiency from the South Indian population. *Indian Journal of Biochemistry and Biophysics*. **31**, 358–360.
27. Rao, P.R. and Gopalan, K.B. (1979). High incidence of silent allele at cholinesterase locus I in Vysas of Andhra Pradesh (S. India). *Human Genetics*. **52**, 139–142.
28. Roychoudhury, A.K. (1976). Incidence of inbreeding in different states of India. *Demography India*. **5**, 108–119.
29. Sanghvi, L.D. (1966). Inbreeding in India. *Eugenics Quarterly*. **13**, 291–301.

30. Schull, W.J. and Neel, J.V. (1972). The effects of parental consanguinity and inbreeding in Hirado, Japan. V. Summary and interpretation. *American Journal of Human Genetics*. **24**, 425–453.
31. Shami, S.A., Grant, J.C. and Bittles, A.H. (1994). Consanguineous marriages within social/occupational class boundaries in Pakistan. *Journal of Biosocial Science*. **26**, 91–96.
32. Sridhara Rama Rao, B.S., Subhas, M.N. and Narayana, H.S. (1977). Metabolic anomalies detected during a systematic screening of mentally retarded cases. *Indian Journal of Medical Research*. **65**, 241–247.
33. Sridhara Rama Rao, B.S. (1995). *PhD thesis*. Indian Institute of Science, Bangalore.
34. Whittaker, M. (1977). “Cholinesterase”, In *Monographs in Human Genetics*. Basel, Karger. **11**, 1.134

4

Human health and our heritage

P.N. Tandon

Department of Neurosurgery, C.N. Centre, AIIMS, New Delhi

*Those who cannot remember the past are
condemned to repeat it*
—Santayana

According to the Oxford Dictionary, heritage is that which is inherited. In addition to the genetic traits on one hand and worldly goods on the other, we inherit culture, i.e., a type of civilisation, which includes our philosophy, religion, ethics, aesthetics, art, and customs. These determine our life style which is now acknowledged as an influence on our health. These evolve in a dynamic fashion over the entire history of a nation. Many customs are neither codified nor empirically tested. However, those which have passed from generation to generation have withstood the test of time and should not be dismissed as 'primitive' or 'native', 'obsolete' or 'old fashioned' under the influence of an alien culture, howsoever powerful that alien society be at a given moment.

Let me quote William and Ariel Durant. "No one, however brilliant and well informed, can come in one lifetime to such fullness of understanding as to safely judge and dismiss the customs or institutions of his society, for these are the wisdom of generations after centuries of experiments in the laboratory of history". It should be obvious that this admonition or warning would be even more relevant for those representing another culture.

Nevertheless, history is replete with examples where, under pressure from claimants of 'higher civilisation', societies have either been forced to or have voluntarily acquiesced their own time-tested customs in favour of unsubstantiated claims of the former. Worse still, it is often done to imitate the alien culture presumed to be better evolved.

At the outset, let me clarify that I am not an advocate of blindly following prevalent customs and traditions for the sake of maintaining *status quo* under the unquestioning belief that "old is always gold". I am certainly not against progress taking advantage of the experience of others. I am against being swept away by such changes without a critical appraisal of the benefits, notwithstanding the strength or superior salesmanship of their advocates. Mahatma Gandhi's prescription in this respect is still valid: "Keep your windows wide open for fresh air from all sides, but make sure you are not blown off your feet".

Physical and mental health and life style

I wish to take this opportunity to support my contention on the basis of some randomly selected, very mundane examples related to the field of health. I crave the indulgence of this august gathering for lack of erudition or high science contents of my talk. I am not

even going to harp upon the heritage of *Ayurveda* or other systems of traditional medicine, notwithstanding the current relevance of at least some of the preachings and practices contained therein. I would nevertheless quote the advice of Jawaharlal Nehru in this connection. "These systems (*Ayurveda* and *Unani*) are repositories of great ancient knowledge deserving our respect, but all this has to be put to scientific test. Every system has to pass the test of scientific approach". This advice is as valuable today as when it was given.

Let me start with the food and eating habits that we have inherited. Traditionally our diet consisted of coarse cereals, whole wheat flour and parboiled rice. Under alien influence the use of whole wheat flour was increasingly replaced by white flour, parboiled rice by polished rice and coarse grains—millets like *jawar*, *bajra*, *ragi makka* (maize), *kala chana* (Bengal gram)—denigrated as the food for the poor or the horses. We sacrificed the dietetic value of these foods in the name of progress. In the bargain we also exposed ourselves to the risk of contracting a variety of diseases including diabetes, chronic constipation and polyposis. Granted that at that time, scientific proof for their superior nutritional value was lacking; it has since been scientifically proved that the so-called coarse cereals have better protein, mineral and fibre content. Those who looked down upon the 'natives' for consuming such cereals are now advertising the benefits of high fibre content diets, while in India we still eat white flour bread. Instead of the traditional cereals for breakfast we are now being submitted to high powered sales pitch about the benefits of corn flakes and potato chips. The scientific community has not yet woken up to undertake critical evaluation of the comparative nutritional value of the new 'fashions' compared to the conventional practices. In the meanwhile, our agricultural practices have made the coarse cereals, which used to be readily available, scarce and beyond the reach of the common man.

Let me support these contentions with the writings of some well-known current nutritional scientists. Denis Burkitt's observations on geographical distribution of diseases from epidemiological data and experimental findings linked a large number of diseases of Western civilisation with lack of fibres in their diet [Burkitt and Trowell, 1975; Trowell and Burkitt, 1981]. Dietary fibres are rich in the important constituents viz., cellulose, hemicellulose, lignin and pectin. A fibre-rich diet restricts calorie intake, slows gastric and small intestinal transit, accelerates the large bowel emptying, and affects the activity of digestive enzymes and release of gastrointestinal hormones. Slower gastric emptying, enhanced hepatic lipogenesis and upregulation of insulin receptors are some of the factors, now confirmed by both animal and human studies, which contribute to beneficial long-term effects. The acute effect of high fibre diet has been shown to result in improved glucose metabolism by reducing post prandial glycaemia. The release of enteroglucagon and formation of propionate by fermentation may also contribute to it [Siddhu et al., 1992; Gee et al., 1996]. These changes result in improved carbohydrate tolerance [Bijlani, 1985; Bijlani et al., 1993]. Viscous, water-soluble variety of dietary fibres have also been reported to lower serum cholesterol and improve lipoprotein profile due to the increase in faecal bile acid excretion.

These observations provide a better understanding of its role in the pathophysiology of constipation, diverticulosis, colo-rectal malignancy, diabetes, atherosclerosis and

cholesterol gallstones. The contribution of dietary fibres in the prevention and treatment of these disorders has now been established on sound scientific footing. The release of insulinotropic hormone and reduced gastric inhibitory polypeptide (GIP) along with lower plasma glucose level, results in lowered plasma insulin level. These observations have obvious implications for prevention and treatment of diabetes [Wapnick et al., 1972; Anderson, 1982].

A few decades ago, the commonly used forms of sugar were brown sugar, jaggery, 'gur', etc. These were subsequently replaced by refined crystal sugar. There was no scientific proof provided while promoting the use of the latter. It has now been established beyond doubt that the more rapid absorption of refined sugar compared to the former results in a sudden elevation of blood sugar, which requires a greater and quicker release of insulin, resulting in adverse effects on the pancreas in the long run. One could add many more examples of the superior nutritional value of many of our traditional dietary practices—unfortunately not yet fully evaluated—which are being replaced by currently fashionable junk food.

Based on eating habits in the West, the requirements for animal proteins were prescribed at such a level that they would cast doubts on the very survival, leave aside sound health, of vegetarians. This in itself should have led to properly conducted scientific investigations. The only study I am aware of on the subject was carried out by one of our distinguished Fellows, Prof. K. N. Sharma. Unfortunately, this study, which provides a scientific answer to this myth, has not received the attention it deserves. In the meanwhile, the ill-effects of such high protein diets are now being acknowledged by their advocates themselves. The advantages of eating vegetables and fruits, which were essential ingredients of our traditional diet, are now the subject of a large number of publications in prestigious scientific journals—alas not by Indians.

It may be of interest to note that dietetics constituted an integral part of *Ayurveda*. Caraka and Susruta Samhita, under the title of '*Ahartattva*', go to great lengths in enumerating, classifying, and ascribing properties to a large number of food items. These texts mention in detail the digestibility, nutritional value and medicinal action of several hundred edible and potable substances of plant and animal origin. True, these descriptions do not provide the chemical constituents or calorific values but only qualitative characteristics. Not for a moment do I advocate a blind acceptance of these values, but certainly, a scientific evaluation is called for. It is amazing that these texts have described fiftyseven tastes derived from the six basic tastes—sweet, acid, saline, pungent, bitter and astringent. This calls for detailed scientific studies, not just for the sake of curiosity but for exploiting the gastronomic potential for commercial purposes.

Some other culturally dependent features of life style

In most old cultures, fasting in one form or other has been advocated. It no doubt became a ritual without an understanding of its rationale. Recent animal studies and some clinical studies have established its beneficial effects on health—especially in delaying senescence.

Most eastern societies, long before the birth of Christ, recognised the benefits of meditation in one form or other—*Yoga* in India, *T'aichi* in China, *Aikido* in Japan. These were based on subjective feelings and empirical observations, not objective measurements of EEG, EMG or blood levels of hormones and metabolites of neurotransmitters. Practised for centuries, these were considered as religious rituals or simply as mumbo-jumbo of some primitive people. Recent investigations have revealed the scientific basis of some of the claims, though not all.

The great importance given to breast feeding in traditional societies can only be gauged from the fact that if mother's milk was not available, a surrogate mother was sought rather than the readily available cow's milk. Of course, the role of breast milk in transmitting immune substances from the mother to the child was not known, nor was the endocrinal basis of delayed return to fertility as a result of prolonged breast feeding. Carried away by sales promotions and influenced, no doubt, by the prevalent fashion among the ruling class, many adopted tin cans. Huge sums of money are now being spent to promote a return to traditional practices.

The derogatory term of 'squatters' was used for Indians. The 'civilised' were supposed to use commodes. It was only through the perceptive mind of Burkitt that the health advantages of squatting were revealed and accepted by the high priests of science and given the dignity of publications in some of the highest impact medical journals.

Let me spend a few minutes on some examples in the realm of therapy. It is obvious that all societies develop a system of popular medicine—beliefs and practices (based on experience, not developed through studies in the labs) used within a family or a community, which are passed on by word of mouth and do not require professional healers. While it will be unwise to adopt these with implicit faith, it behoves the scientific community to investigate these claims using the latest techniques available. The antimalarials derived from Cinchona were not developed by scientific rigours of drug development today, nor did the use of aspirin go through these birth pangs. The various uses of neem and turmeric were already known long before their active principles were isolated. We have missed valuable opportunities to utilise the existing wealth of information in our traditional system of medicine. The scientific community, proud of its links with modern science, was ill-prepared and unwilling, often considering it below its dignity, to involve itself with these 'unscientific' systems. Recent developments have demonstrated that, due to our ignorance or arrogance, we missed a great opportunity. It is not too late even now to exploit these treasures scientifically, before others claim patent rights on more of these.

Time does not permit me to describe several other such beneficial practices, from our traditional life style, not all still submitted to scientific proof. I would quote just two other examples from other parts of the world which illustrate the influence of life style in prevention of diseases. A prospective study of the incidence of, and mortality from, coronary heart disease was conducted in Finland, where one of the highest mortality rates from this disease was recorded. From 1970 onwards they observed a progressive decrease in the mortality rate. This was ascribed to primary preventive effects of improved life styles and concomitant risk factor changes [Salomaa et al., 1992]. Even more revealing is a study carried out in Australia where marked improvement in carbohydrate and lipid metabolism was observed in diabetic Aborigines from Western Australia when

they reverted to their hunting-gathering existence in their traditional community for seven weeks. At the end of this period, it was noted that the major metabolic abnormalities of Type II diabetes were either greatly improved or completely normalised [O'leo, 1984].

These examples should convince skeptics that it is unwise to discard one's heritage without scientifically evaluating its rationale. Today we have tools and techniques to do so. I hope I am not mistaken for a parochial nationalist or a chauvinist when I suggest that the seeds of some of the newly emerging disciplines like ecological medicine, geographical medicine or the concepts of psychoneuroimmunology can be found in our rich heritage. We are the inheritors of a rich cultural heritage and traditional wisdom. The scientific community should evaluate these and utilise whatever stands the test of critical appraisal, for the benefit of advancement of knowledge and welfare of our people. This is not to advocate living in our fossilised past, but to gain from the beliefs and practices which have evolved over many millennia. Its continued neglect by the scientific community can only lead to its uncritical use by lay practitioners or exploitation by enterprising foreigners. There is today an increasing risk of being swamped by the invasion of 'ultra modernism'.

Let me close by borrowing a statement by Einstein, no doubt made in another context, yet relevant to the present subject. "Let all of us therefore summon our strengths. Let us be tirelessly on guard lest it be said later of the intelligent elite of this land: Timidly and without struggle they surrendered the heritage handed down to them by their forefathers—a heritage we were not worthy of"

References

1. Anderson, J.W. (1982). Dietary fiber and diabetes. In G.V. Vahouny and D. Kritchsky, (eds.). *Dietary Fiber in Health and Disease*. Plenum Press, New York. 151-167.
2. Bijlani, R.L. (1985). Dietary fibre: Consensus and controversy. *Progress in Food and Nutrition Science*. 9, 343-393.
3. Bijlani, R.L., Narain, J.P., Shukla, K. et al. (1993). Glycaemic and metabolic responses to a traditional cereal-legume mixture. *Int. J. Food Sc. Nutr.* 44, 243-251.
4. Burkitt, D.P., Trowell, H.C., (eds.). (1975). *Refined carbohydrate foods and disease. Some Implications of Dietary Fibre*. London Academic Press.
5. Cleave, T.L. and Campbell, C.D. (1966). *Diabetes: Coronary Thrombosis and the Saccharine Disease*. Bristol, John Wright.
6. Gee, J.M., Lee-Finglas, W., Wortley, G.W. and Johnson, I.T. (1996) Fermentable carbohydrates elevate plasma enteroglucagon. *J. Nutr.* 126, 373-379.
7. O'leo, K. (1984). Marked improvement in carbohydrate and lipid metabolism in diabetic Australian Aborigines after temporary reversal to traditional life style. *Diabetes*. 33, 596-603.
8. Siddhu, A., Sud, S., Bijlani, R.L. et al. (1992). Nutrient interaction in relation to glycaemic and insulinaemic response. *Indian J. Physiol. Pharmacol.* 36, 21-28.
9. Trowell, H.C. and Burkitt, D.P. (1981). *Western Diseases, their Emergence and Prevention*. Edward Arnold, London.
10. Salomaa, V., Arstila, M., Kaarsalo, E. et al. (1992). Trends in the incidence of and mortality from coronary heart disease in Finland 1983-88. *Am. J. Epidemiol.* 136, 1303-1315.
11. Wapnick, S., Wicks, A.C., Kanengoni, E. and Jones, J.J. (1972) Can diet be responsible for the initial lesion in diabetes. *Lancet*. 2, 300-302.

Molecular genetic markers in the study of human heritage

Shama Barnabas and C.G. Suresh

Division of Biochemical Sciences, National Chemical Laboratory, Pune

Introduction

Undoubtedly, living organisms, or more precisely the extant species, provide the most tangible data for the study of evolution of the biosphere. However, fossils of the extinct species provide concrete evidence of past life when reconstructing the evolutionary history of living organisms. Palaeontology has played a major role not only in understanding biological evolution in general, but also in deciphering the history of human evolution which led to the emergence of modern man. Accurate dating methods developed for assessing the age of fossils have added to the authentication of the chronological order in which different species appeared on earth. One major limitation of fossil studies is that the preservation of fossil records in the Earth's crust is more an exception than the rule.

Human evolution can be traced in the fossil record from the Miocene (25–5.5 million years ago, or myr) apes which showed extensive dispersal or radiation into different parts of the world. Two lineages arose from the African hominoids; one gave rise to the gorilla, chimpanzee and man, while the other gave rise to the orangutan in Asia. From the African hominoids evolved the hominoids *Aridipithecus ramidus* (4.4 myr), *Australopithecus anamensis* (4.2–3.9 myr), *Australopithecus afarensis* (3.9–2.3 myr) etc. These were found in eastern and southern Africa. From these hominoids evolved two lineages. One included *A. africanus* (3.2–2.3 myr), *Homo ergaster* (1.9 myr from Africa and China) and *Homo erectus* (1.6 myr from Africa, Java and China). The other lineage included the more robust *A. robustus* (1.9–1.6 myr) which were also found in Africa. *Homo erectus* was fully erect, had manipulative hands with thumb opposability and precision grip. He was able to make tools and travelled out of Africa to other parts of the world. Intermediate fossils between *H. erectus* and *H. sapiens* are found in Africa. *Homo sapiens* is the archaic man who made home bases, gathered and shared food and used fire. From the archaic man evolved two lineages—the Neanderthal man who lived in Europe and Southwest Asia between 100,000 to 30,000 years ago, and the modern man, *Homo sapiens*.

Evolution of modern man is also associated with the emergence of different 'tool industries', from the shaping of stones to the manufacture of modern computers. Archaeology, the study of human artifacts from the past, has helped in the detailed

study of global human migrations, expansion of populations, and settlements of modern man and his immediate ancestors. But a limitation of these studies is that cultural remains of man's ancestors are often not associated with human remains. Similarly, the skill developed by human beings in communication has also turned out to be a tool worth investigating. Languages, both written and spoken, have been developed as a means of communication, and different populations have left their own imprints on the languages used. Linguistic data could thus help in understanding population relations.

Advances in molecular biology have changed the whole orientation of evolutionary studies. Every organism carries DNA which is inferred to exhibit compositional changes (mutations) which are transferred from generation to generation. In fact all evolution could in turn be traced back to the evolution of DNA. If we assume that this molecule is constantly and uniformly changing in terms of the arrangement of constituent bases, and the changes are not under any external control, then this provides a useful tool in the construction of phylogenetic relationships between organisms. The evolution of nuclear DNA is slow when compared to the time scale of human evolution. Also the nuclear DNA is inherited from both parents and undergoes recombination, making it difficult to trace the history of any particular segment of the DNA. Nevertheless, the study of nuclear DNA, in conjunction with archaeological and linguistic data, has contributed significantly to the present-day understanding of the history of several world populations [Cavalli-Sforza et al., 1988].

In the late 1970s, researchers identified an extrachromosomal DNA, the mitochondrial DNA (mtDNA), which was more suitable than nuclear DNA in the evolutionary studies of closely related species and in the study of diversity of intra-species populations [Brown et al., 1979] and has been used as an effective tool in understanding the genealogical history of human species [Cann et al., 1987; Merriwether et al., 1991; Vigilant et al., 1991].

Considering all the reported studies using molecular genetic markers till now, it is evident that only small segments of the culturally diverse Indian population have been covered in each of these studies. Nevertheless, these studies have succeeded in bringing out our relationship with some of the other populations of the world. Many questions regarding the occupation of the Indian subcontinent by our species and various migrations are still left unanswered. Thus, a concerted effort is required, not only to study a wider spectrum of Indian population using molecular genetic markers, but also to analyse this data in the light of the data obtained from archaeological, palaeontological and linguistic studies.

Studies using DNA genetic markers and sequences

In one of the first attempts to construct the human phylogeny using molecular markers, 15 populations were studied using gene frequencies of 20 alleles from 15 major blood group systems [Cavalli-Sforza et al., 1988]. This study was extended with the addition of more genes, including histocompatibility locus antigens (HLA) which did not alter the original phylogenetic tree very much. Nei (1985) has studied 18 populations, which he classified as belonging to Caucasian, Negroid and Mongoloid, using gene frequency

data for 62 protein loci and 23 blood group loci. Using genetic distance estimates he has shown that the Caucasian and Mongoloid races are closer to each other than to the Negroid. This study has also reported an estimate of divergence time of the three races. In another study [Wainscoat et al., 1986], eight world populations were studied (using restriction enzyme sites in the β -globin gene cluster) and the phylogenetic tree obtained from this study was more or less similar to that of Nei's. Indians were one of the populations studied here and were placed between Mongoloids and Caucasians. Cavalli-Sforza et al. (1988), in their effort to reconstruct human evolution, have brought together a large collection of gene frequencies available in the literature for 42 populations based on 120 alleles (alleles are two or more genes representing different realisations of the same character such as blue or green colour of the eye, or round or wrinkled appearance of a seed). Their analysis again confirmed an early African-non-African split. This study placed the Indian population along with the Caucasians. In a further effort they tried to support the conclusions drawn from the genetic studies with linguistic data [Cavalli-Sforza et al., 1992].

Molecular biology has recently provided a powerful method to compare the similarity or identity between two DNA sequences and thus establish their relatedness. This involves cutting the DNA molecules into well-defined fragments (using enzymes called restriction endonucleases), lining up the fragments of the DNAs and comparing the fragment lengths as 'signatures'. Called restriction fragment length polymorphism (RFLP), this method is now in standard use to establish the relatedness of two genes or DNA molecules.

A comparative study of nine populations using 80 nuclear DNA by the RFLP method has been reported in a recent paper [Poloni et al., 1995]. This study also confirms the higher genetic diversity in the African population. The clustering of African and European populations seen in the phylogenetic tree here, were similar to those reported in previous studies. However, the Mongoloids showed a branching into East Asians and Oceanians. It is suggested that the two separate branches may reflect two distinct migrations along two separate routes, one to the north of Himalayas and the other to the south. Since no Indian population was included here, the position of Indians with respect to this type of study cannot be ascertained. Thus the two main observations based on the studies of various gene frequencies are that the differences between racial groups are smaller than those within each group and the gene frequency differences of the Africans are the largest.

Tracing ancestry through maternal inheritance

When it was discovered that the mitochondrial DNA is a suitable molecule for the study of closely related species and individuals within species, it provided the right impetus to the study of human evolution using molecular genetic markers. Human mtDNA is an extrachromosomal DNA consisting of 16,569 base pairs (bp) arranged in a covalently linked circular loop. Theories on the origin and evolution of mtDNA in eukaryotes are still disputed. There are two main advantages in using mtDNA as a tool in the evolutionary studies of humans. First is that the human mtDNA, rather the mammalian mtDNA in general, is maternally inherited [Giles et al., 1980]. Thus mtDNA is devoid of the mixing

of genes from both parents (which is the case with nuclear DNA that obscures the history of individuals). Secondly, vertebrate mtDNA is shown to mutate or evolve five to ten times faster than the nuclear DNA [Brown et al., 1979; Vawter and Brown, 1986]. Thus, the study of human mtDNA provides a time clock in the stages of evolution, as well as a magnified view of the diversity present in the human gene pool. Among the mutations, transitions outnumber transversions and base substitutions are far more common than additions or deletions. The mutation rate is not uniform throughout the mtDNA. A 1122 bp non-coding region which controls transcription and replication is the most variable region [Rienzo and Wilson, 1991]. In this region, termed the D-loop (for displacement loop), a segment spanning the first 400 bp accounts for almost two-thirds of the nucleotide substitutions observed in sequence studies.

Humankind arose out of Africa!

Earlier studies of the world populations were based on RFLP studies on human mtDNA. Simultaneous developments in the theoretical analysis [Nei and Li, 1979] have facilitated phylogenetic inference from restriction fragment data. The sequencing of human mtDNA by Anderson et al. (1981), and the introduction of maximum likelihood methods for restriction site analysis [Nei and Tajima, 1983] have paved the way for high resolution studies of mtDNA and derive more accurate phylogenetic trees from existing data. One of the first such studies sampled 21 individuals belonging to diverse races and geographical regions using 18 restriction endonucleases [Brown and Goodman, 1979; Brown, 1980]. The analysis of the data suggested that *Homo sapiens* could have passed through a severe population constriction some 180,000 years ago. In a subsequent study using endonuclease Hpa I in 235 individuals from five ethnic groups [Denaro et al., 1981], it was suggested that modern man arose in Asia somewhere between 50,000–100,000 years ago. In an extended study, 200 samples were subjected to digestion by four more endonucleases [Johnson et al., 1983]. In this study—one of the first attempts to infer the phylogeny of mtDNA types—a tree was drawn using parsimonious methods based on the nucleotide substitutions at the endonuclease restriction sites. In their phylogenetic tree, the 35 distinct mtDNA types were found to separate into three geographically distinct groups (African, Caucasian and Oriental).

In the last one decade or so, several studies on individual populations using mtDNA polymorphisms based on restriction fragment analysis were reported. Two such studies are worth mentioning. In one of them, mtDNA from 147 individuals belonging to five geographic regions was mapped using 12 restriction enzymes [Cann et al., 1987]. It was found that the Africans, among the five populations studied, showed the greatest genetic variation, followed by Asians while Australians, Caucasians and New Guineans were less diverse. Their phylogenetic tree relating the 133 mtDNA types, built using the parsimony method, had two primary branches, one composed entirely of Africans and the other including all the five populations. In the absence of a proper outgroup, the root was placed at the midpoint of these two branches. By assuming the mean rate of divergence for human mtDNA to be about 2 to 4% per million years, the study suggested that the common ancestor of all surviving mtDNA types existed 140,000–290,000 years ago. The authors

also suggested that the origin of the common ancestor would be in Africa. Interestingly, ever since this paper appeared, it has generated extensive debate regarding the region and evolutionary time scales of human origin [Darlu and Tassy, 1987; Templeton, 1991; Goldman and Barton, 1992].

In a more elaborate study of mtDNA using restriction enzymes, 3065 samples from 62 geographic regions were included for analysis [Merriwether et al., 1991]. The strategy of the authors was to analyse a larger sample size using a core set of six restriction endonucleases in order to identify polymorphic restriction sites. They classified the individuals into four major ethnic groups: Asian, Caucasian, African and Amerindian. Their UPGMA (unbiased pair group method with arithmetic averages) tree for the 149 haplotypes showed that Africans span the deepest branch of the tree. Also, the calculations showed that Africans had the highest diversity. Thus this study also concluded that the human species probably originated in Africa.

The RFLP and high resolution site mapping studies using even a larger number (12) of restriction enzymes could include only 9% of the 16,559 bp human mtDNA genome for analysis [Cann et al., 1987]. Even with the advancement of sequencing techniques, the sequencing of the whole mtDNA corresponding to several samples still remained a formidable task. It has already been shown that the major non-coding or control region is the most variable part of human mtDNA [Aquadro and Greenberg, 1983]. The majority of nucleotide substitutions are in the first 400 bp of this region [Rienzo and Wilson, 1991]. Thus, most of the sequence studies concentrated on this 'hypervariable region' of the mtDNA.

Here also the first comprehensive study of mtDNA D-loop sequences belonging to people of diverse geographic origin was carried out by Allan Wilson's group [Vigilant et al., 1991]. Sequences from 189 samples were surveyed and 135 mtDNA types were identified. A genealogical tree relating these mtDNA types has been constructed using the parsimony method. The rooting using common chimpanzee sequences as an outgroup divided the tree into two primary branches, one consisting of only African mtDNA types, and the other containing all types. Thus the authors substantiated their earlier finding, based on RFLP high resolution studies, that Africa could be the continent where man's common ancestor originated. Based on the rate of mtDNA evolution, calibrated using chimpanzee and human sequences, the age of the common ancestor was placed between 166,000 and 249,000 years. A subsequent study [Horai et al., 1995] based on the complete sequences of different hominoid mtDNAs lent support to this hypothesis. The age of the common ancestor was inferred as 143,000 years with ambiguity of 18,000 years. Subsequently, several sequence studies on populations from various geographical locations have been reported [Mountain et al., 1995; Bertranpetit et al., 1995]. However, none of them has disputed the model of the African origin of modern man.

Tracing patrilineage

Just as maternal lineages can be traced through the mtDNA polymorphisms, the paternal lineages can be traced through the male specific part of the Y chromosome. There are differing views regarding Y chromosome variation. Some investigators believe that the

variation on the Y chromosome is reduced compared to autosomes and the X chromosome due to selection of a favorable mutation in the non-recombining part of the Y chromosome. A study [Whitefield et al., 1993] of 100 kb from the non-recombining part of the Y chromosome from 5 humans and 1 common chimpanzee estimates a coalescence time which is more recent than that obtained from mtDNA studies and explains it by a selective sweep of an advantageous Y chromosome of large scale migrations of males. Another study [Hammer, 1995] which is based on sequencing of a 2.6 kb fragment that encompasses a polymorphic Alu insertion has been carried out in 16 humans and 4 chimpanzee Y chromosomes, and does not find any evidence for a strong selective sweep on the Y chromosome. It estimates a coalescence time back to a common Y chromosome to be 188,000 years which is comparable to that derived from mtDNA studies.

Use of further details in DNA sequences for more rigorous analysis

Other more recent tools for the study of human population diversity are the various hypervariable loci which are also called variable numbers of tandem repeats (VNTRs). VNTRs are characterised by a large number of alleles, resulting in high heterozygosity per locus. The VNTR polymorphism is concerned with variation in repeat sequences usually found in the non-coding DNA. Alleles may vary due to different numbers of copies of the repeat unit in a particular DNA fragment. A single-locus probe (SLP) made through the use of PCR (polymerase chain reaction) may identify allelic types which represent different copy numbers (or the total length) of the repeat units of the tandemly repeated DNA sequence. A multi-locus probe (MLP), on the other hand, exhibits a DNA fingerprint made up of multiple bands which represent copy number variations of similar sequences at an unknown number of loci in different parts of the genome.

A number of studies are being carried out utilising repetitive DNA polymorphism. A recent study of repetitive DNA or micro-satellite loci supports the deep split between the African and non-African populations [Goldstein et al., 1995]. A study of dinucleotide repeat loci located on human chromosome 13q showed that, at a given locus, the most frequent alleles were shared by all human populations studied [Deka et al., 1995a], though there was substantial variation in allele frequencies at different loci. Another study of genetic distance in 15 human populations based on six short tandem repeats recognised three distinct clusters: Africans, Caucasians and Mongoloids [Deka et al., 1995b].

The Alu elements which are the most common mobile short interspersed elements (SINEs) in the human genome are also being used to study human diversity. They are present in nearly one million copies, forming more than 5% of the human DNA [Hwu et al., 1986]. They are about 300 nucleotides in length [Rinehart et al., 1981] and are made up of a tandem arrangement of two related but non-identical left and right monomers [Weiner et al., 1986]. The Alu elements appear to be derived from an internally

deleted 7SL gene [Ullu and Tschudi, 1984] and have fused to form the dimeric Alu element [Jurka and Zuckerkandl, 1991]. They appear to get transposed through an RNA intermediate.

It is possible that the Alu families were produced by the radiation of a limited number of master sequences and different master sequences were transpositionally active at different times of the evolution. Most of the Alu elements amplified in the primate line 30–65 myr ago and the amplification process still appears to be active, HS/PV or SB1 [Batzer et al., 1990] and SB2 [Jurka, 1993] being two of the youngest subfamilies. Their amplification started at the time of the divergence of humans and great apes. The SB1 subfamily is transpositionally active at present [Wallace et al., 1991] and is made up of about 2000 elements [Matera et al., 1990].

The Alu elements' preintegration sequences are unique and can be developed as sequence tagged sites (STS) for the study of human genetic diversity. Some recent Alu element studies have yielded interesting results. A study [Batzer et al., 1996] of six polymorphic Alu insertions in 14 human populations from different continents indicates that these polymorphic Alu insertions probably originated in Africa. This study also found the European populations to be more homogeneous compared to other populations.

Another significant study [Tishkoff et al., 1996] which is the largest study of nuclear DNA, examined 1600 people in 42 populations. The DNA is a fragment of chromosome 12 which consists of two segments present a short distance from each other. There is a slow-evolving Alu element and a faster evolving short tandem repeat polymorphic segment (STRP). The Alu element has two forms, a shorter form and a complete form, whereas the STRP has twelve forms. It was found that outside Africa, only the truncated Alu element dominated. In Ethiopia and Somalia there are some more forms whereas in sub-Saharan Africa there was much more variation. Thus it was suggested that some variation was lost in Northeast Africa and a small population from Africa migrated to the rest of the world. In this migrating population, the truncated Alu form was linked with the 90 bp STRP. Since the deletion is not found in the African apes it would have occurred within the last 5 million years on a chromosome having the 90 bp STRP which is most commonly associated with this deletion. In Africa there has been more time for the STRP to mutate to other forms but in the rest of the world the link between the 90 bp STRP and the truncated Alu element is much stronger. If it is assumed that the mutation rate is more or less constant, it appears that humans migrated out of Africa more recently, thus explaining the low variation seen in the Alu element and the STRP. This migration is suggested to have occurred 100,000 years ago. This agrees with dates derived from mtDNA studies and Y chromosome studies. There is no doubt that a clearer picture of human origin will emerge only after more genetic loci are studied.

Models of human evolution: Africa and the 'Garden of Eden'

There are two conflicting views on the origin of modern man. Most of the genetic data, including that from mtDNA studies, supports an African origin of modern man, with a subsequent spread of the species all over the world, replacing *Homo erectus* [Wilson and Cann, 1992]. This view has been contested by a section of anthropologists who

point out that the fossil evidence indicates a regional continuity of the features shown by *Homo sapiens* derived from *H. erectus* already settled in these regions [Thorne and Wolpoff, 1992]. According to the former view, the distinctive human racial features in different geographical locations have independently evolved in *H. sapiens*. Whereas, according to the latter hypothesis, the regional variations in humans are the result of continuous local evolution leading to *H. sapiens* from regional populations of *H. erectus* over a longer period of time. A more recent opinion, 'the Garden of Eden' model, suggests that the human populations diverged from an initial source (probably Africa), separated from each other about 100,000 years ago but did not undergo expansion till tens of thousands of years later [Rogers and Jorde, 1995].

Studies of Indian populations

In order to sample the ancestral diversity of our country, we have studied 100 Indians from fourteen language groups [Barnabas et al., 1996a, 1996b]. The fourteen languages are Hindi, Marathi, Sindhi, Gujarati, Urdu, Bihari, Punjabi, Bengali, Marvari, Konkani, Tamil, Telugu, Malayalam and Kannada. The first ten languages are derived from Indo-European languages and the last four are Dravidian languages. There were practical difficulties in studying a sufficiently large number from each group, but during our study we found that, based on mtDNA data, meaningful conclusions can be drawn by grouping individuals into Indo-European language and Dravidian language speakers. We also found that the population belonging to Maharashtra, from which we have studied a statistically sound number, showed lower diversity in comparison to populations in the north and south. Thus we decided to sample the data into three populations: North Indians, South Indians and Central Indians (Maharashtrians).

We have studied mtDNA using the same set of six restriction enzymes (HpaI, BamHI, HaeII, MspI, AvaII and HincII) which have been used in the study of other world ethnic groups and for which considerable data exists, in order to compare and discern possible relationships of the Indian populations. Data from an earlier study [Semino et al., 1991] of North Indians has been used along with ours for the calculation of nucleotide diversity as well as for the construction of phylogenetic trees. 29 mtDNA types were identified from a sample population of 145 individuals (Table I). Information from 63 sites in the mtDNA sequence recognised by four, five and six cutter enzymes was included in the calculation. Nucleotide diversity was calculated by the maximum likelihood method of Nei and Tajima (1983). A measure of homogeneity in the populations was obtained, following Nei's (1973) summation of the squares of the relative frequencies of each type of mtDNA in the population.

Largely Caucasian ancestry

Nucleotide diversity in percentage was 0.18 for Indians as a whole (0.21 for North Indians, 0.20 for South Indians and 0.12 for Maharashtrians) and 0.28 for Caucasians, indicating that the Indian population may be younger than the Caucasian population. The nucleotide diversity calculated from North and South India separately was almost equal.

The F index [Johnson et al., 1983] calculated from the frequencies of different mtDNA types was 0.47, 0.52 and 0.61 for South, North and Central Indian populations respectively. From the F index calculation, the South Indians appear to be more diverse than the North Indians; but the sample of South Indians is not sufficient to reach any firm conclusion. It is also apparent that the Central Indian population of Maharashtra is more homogeneous, indicating that it may be a recently expanded population.

Restriction site sequences were used for inferring the phylogenetic relationships among the 29 mtDNA types identified, employing the maximum parsimony method. Here we considered the loss of a restriction site to be due to a transition (preferred over a transversion) of any one of the nucleotides in the site which does not change the coded amino acid. 600 bootstrap replicates of the input sequences were carried out to arrive at the consensus trees. All the parsimony calculations were done and dendrograms drawn using the PHYLIP package Ver. 3.5 [Felsenstein, 1993].

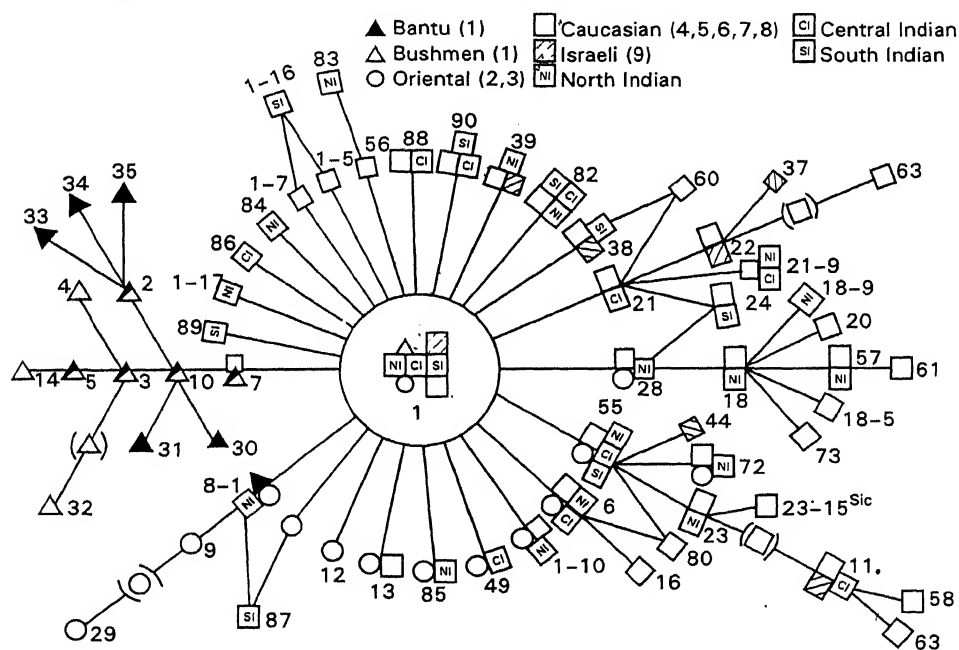


Fig. 1 Phylogeny of the 29 Indian mtDNA types constructed according to Johnson et al. (1983) and placed along with mtDNA types of other world populations (taken from Barnabas et al., 1996b)

The 29 mtDNA types found in the Indian population were used to build a parsimony tree derived from Johnson et al., (1983) and other workers [Bonne-Tamir et al., 1986; Santachiara Benerecetti et al., 1988], revised in the light of our observations (Fig. 1). The phylogenetic trees derived from the restriction site sequences using UPGMA (tree not shown) and parsimony methods (Fig. 2) showed the clustering of mtDNA types seen along the longer branches in Fig. 1. The common lineage shared by the Indian

population with other world populations is evident from the overwhelming presence of the common mtDNA in Indians as well as mtDNA types such as 8-1 shared with Africans and Asians and types 1-10, 6, 72, 28 and 55 shared with Caucasians and Asians. The Indian mtDNA types included twelve Caucasian mtDNA types (23, 39, 18, 57, 24, 38, 11, 21, 88, 21-9, 90, 82). Out of the 8 unique Indian mtDNA types, three (18-9, 83, 1-16) can be derived from the Caucasian types by single mutations. This observation clearly indicates a relationship between Indians and Caucasians as has been suggested earlier [Semino et al., 1991; Soodyall and Jenkins, 1992; Mountain et al., 1995].

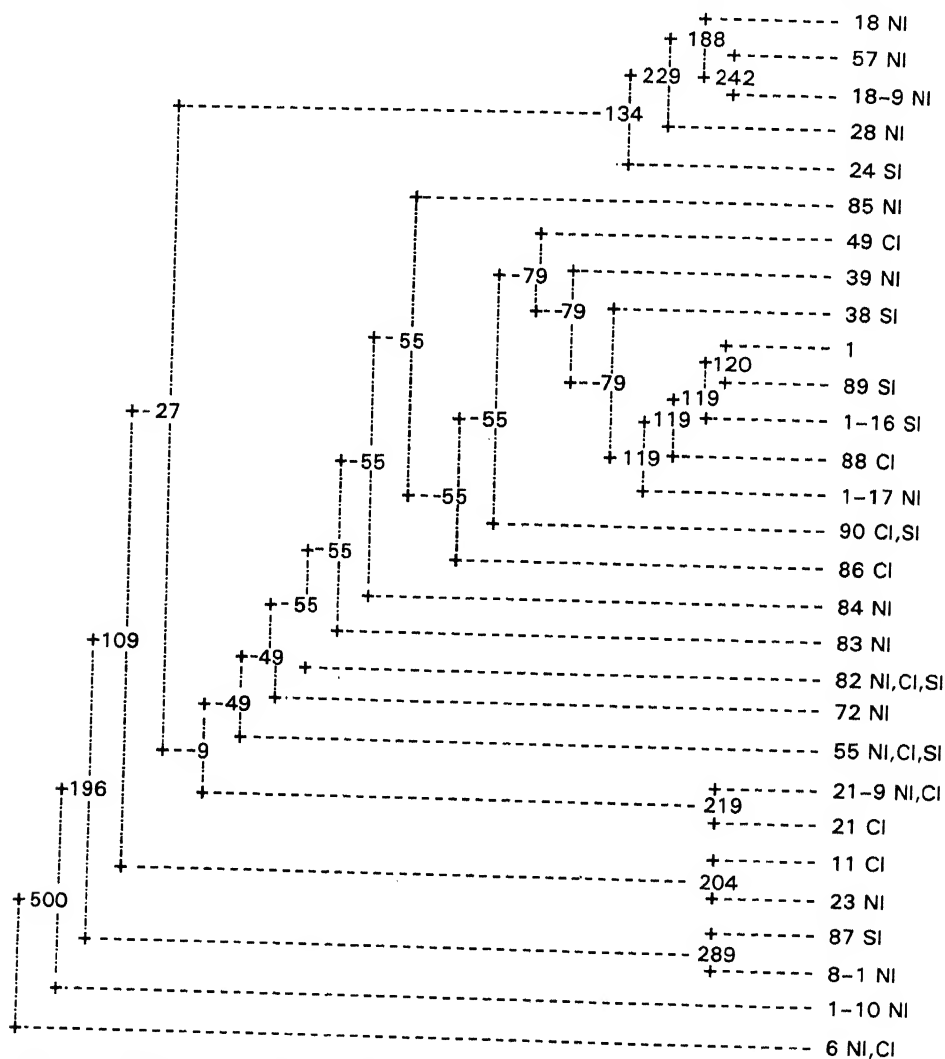


Fig. 2 Parsimony tree of the 29 Indian mtDNA types shown in Table 1 (taken from Barnabas et al., 1996b)

Table 1 Frequencies of *mtDNA* types in North Indians, Central Indians (Maharashtrians), and South Indians compared with Caucasians, Israelis, Asians and Africans

Mitochondrial DNA Types*	North Indians N = 67	Central Indians N = 50	South Indians N = 28	Total Indians N = 145	Caucasians N = 568	Israelis N = 78	Asians N = 244	Africans N = 74
1	71.64	78.0	67.86	73.10	65.84	47.43	53.27	14.9
1-10	1.49			0.69	0.18		0.82	
1-16			3.57	0.69				
1-17	1.49			0.69				
*6	1.49	2.0		1.38	5.63	19.23		
8-1	2.98			1.38			13.36	2.7
11		2.0		0.69	1.76	1.28		
18	2.98			1.38	8.00			
18-9	1.49			0.69				
21		2.0		0.69	3.00			
21-9	1.49	2.0		1.38	0.18			
*23	1.49			0.69				
24			3.57	0.69	0.35			
28	1.49			0.69	0.35		0.82	
38			3.57	0.69	0.88	1.28		
39	1.49			0.69	0.35	1.28		
49		2.0		0.69			0.41	
55	1.49	2.0	7.14	2.76	2.29		7.79	
57	1.49			0.69	1.90			
*72	1.49			0.69	0.18			
*82	1.49	2.0	3.57	2.06				

contd.

Table 1 *contd.*

Mitochondrial DNA Types*	North Indians N = 67		Central Indians N = 50		South Indians N = 28		Total Indians N = 145		Caucasians N = 568		Israelis N = 78		Asians N = 244		Africans N = 74	
83	2-1-1-1-29 ^{hin} -2	1.49					0.69									
84	2-0 ^{hin} -1-1-30 ^{hin} -2	1.49					0.69									
85	2-1-1-7 ^{ind} -18 ^{hin} -2	1.49					0.69									
86	2-1-1-1-17 ^{ind} -1-2		2.0				0.69									
87	1-3-1-1-9-1				3.57		0.69									
88	2-1-1-1-7*-2		2.0				0.69									
89	2-1-1-1-18 ^{ind} -1-2				3.57		0.69									
90	2-1-1-1-6*-2		4.0		3.57		2.06									

*The enzyme morphs in the mitochondrial DNA types are indicated in the order: HpaI, BamHI, HaeII, MspI, AvalI and HincII.

*mtDNA types 6 and 23 have been reported (Johnson et al., 1983) in Asians and Caucasians, respectively.

*mtDNA type 72 has been reported in the Japanese.

*mtDNA type 82 has been reported in Sardinians.

*Taken from Barnabas et al. (1996b).

Some Asiatic admixture

Indians share mtDNA types 8-1, 85 and 49 with Asians. Mitochondrial DNA type 87 found in South Indians is a unique Indian mtDNA type and can be derived from 8-1 (1-1-1-1-1-1). The rare mtDNA type 85 found in North Indians earlier [Semino et al., 1991] and the type 49 found in Maharashtrians are shared with Tharus of Nepal who are reportedly related to Asians [Brega et al., 1986]. Thus the presence of Asian mtDNA types (not found in Caucasians) among Indians could be due to an Asian admixture. The mtDNA type 1-1-1-1-1-1 which is less frequent among Asians compared to the type 1-1-2-1-1-1 was found in the sample of 145 Indians discussed here. Most of the northeastern states (where the Asian admixture is very apparent) were not sampled in the present study. It will be reasonable to assume that a very early migration of Asians, before the 1-1-2-1-1-1 mtDNA type had evolved and reached its present frequencies among the Asians, would have brought the 1-1-1-1-1-1 mtDNA type to India. Perhaps the Austro-Asiatic language speaking tribals found in some parts of India who are regarded as having originated from South China could be considered these ancient migrants. It is also possible that the Austro-Asiatic language speakers came to India from the Mediterranean region [Bhasin et al., 1994] and together with the linguistic evidence for an Asiatic connection of the Austro-Asiatic language speakers, it can be postulated that there was a wave of migration from Africa to Asia through the Indian subcontinent.

From Fig. 1 it is also apparent that the three Indian populations do not share the unique mtDNA types with one another. Mitochondrial DNA type 55 which is shared by all the three Indian populations is an Asian-Caucasian type and 82, which is again shared by all the three Indian populations, is a Caucasian type. In Fig. 1 the North and South Indian populations do not share any other mtDNA types except these two. Anthropological studies also support this view [Singh et al., 1994].

Is the South Indian population an earlier Caucasian migrator?

It can be seen from the parsimony tree that the South Indian mtDNA types shared with the Caucasians are placed comparatively closer to the central common mtDNA type in terms of the number of mutations. On the other hand some mtDNA types shared by North Indians and Caucasians are placed further away from the common mtDNA type, along the Caucasian branch. Thus it is possible that the population in the South is an earlier Caucasian migration while that in the North is a mixture with a later migration.

There is support of this idea of two populations, from linguistic data. The Dravidian languages are spoken in the South whereas the North Indian languages are derived from Indo-European languages. One of the areas where agriculture originated is the Zagros region of Iran and Iraq. From this area it spread towards the Southeast and East, into Asia. A relationship has been found between the Elamite language which was spoken in Elam (present Khuzistan and southwestern Iran) and the Dravidian languages of

India [Renfrew, 1989]. Thus a migration of farmers from the Zagros region could have brought the ancestor of Elamite and Dravidian languages to India and Pakistan. The Brahui language of Baluchistan has some resemblance to Dravidian languages [Renfrew, 1989]. The nucleotide diversity values for South Indians suggest that this Caucasian migration into the Indian subcontinent might have been earlier than the 6500 BC suggested for the origin of Indo-European languages.

There are two regions which are regarded as the homeland of Indo-European languages—the steppes area north of the Black Sea in Russia [Childe, 1926], and the Anatolia region which is now part of Turkey [Renfrew, 1989]. The Indo-European languages could have spread and reached India through the Kurgan invasions by nomadic pastoralists or the local migrations of farmers with the spread of agricultural economy [Renfrew, 1994]. This may have resulted in the second mixture of Caucasian type of mtDNA in the northern part of the country.

A fossil (the Narmada man) belonging to the Middle Pleistocene has been found in Madhya Pradesh and indicates that the Indian subcontinent was populated as far back as Middle Pleistocene. The fossil was a specimen of *Homo sapiens* with an age less than 0.73 myr [Kennedy et al., 1991]. Archaeological evidence indicates that the Indian subcontinent was populated around 0.6 myr before present (BP) [Mishra et al., 1995]. Palaeolithic cultures are found in India from 600,000 to 10,000 years BP. Upper Palaeolithic (40,000 years) culture flourished in different parts of the country and probably represents the activities of modern man (*Homo sapiens sapiens*) [Misra, 1989].

Our study of Indian mtDNA types is not indicative of an ancient population based on the diversity values obtained by us; rather it indicates a population which shares a common lineage with the Caucasians and Asians. Thus, perhaps migrations of modern man into the Indian subcontinent from a common stock shared with the Caucasians would have given rise to the present-day Indian populations. Our study does not include the Indian tribals but demonstrates that the present-day non-tribal majority population does not represent the indigenous population.

A recent study [Bamshad et al., 1996] of 36 Indians from four castes in Andhra Pradesh, based on D-loop sequencing, interrelated the Indians with other world ethnic groups and found the caste populations to cluster more often with Africans than Asians or Europeans, indicating an admixture with Africans.

Conclusion

Palaeontology, anthropology, archaeology, linguistics, classical genetic marker and modern molecular genetic studies have contributed to the knowledge of Indian human heritage. There were efforts [Singh, 1993] to bring together all the data from the above studies in order to draw firm conclusions on the populating of the Indian subcontinent. Though the Indian population exhibits much more cultural and linguistic complexity compared to many regions of the world, very few studies have been carried out using molecular genetic markers. Indeed, some of the recent mtDNA studies on small Indian samples have succeeded in revealing their relationships with other world populations. Our own studies, using modern molecular biology techniques on Indian samples drawn

from different geographic regions, have also contributed to the knowledge of intrapopulation and interpopulation relationships between Indians and other world populations. Molecular genetic studies using modern techniques should contribute in a big way to the knowledge of Indian human heritage and perhaps will be able to answer some of the questions raised by studies from other disciplines.

References

1. Anderson, S., Bankier, A.T., Barrell, B.G., de Bruijn, M.H.L., Coulson, A.R., Drouin, J., Eperon, I.C., Nierlich, D.P., Roe, B.A., Sanger, F., Schreier, P.H., Smith, A.J.H., Staden, R. and Young, I.G. (1981). Sequence and organisation of the human mitochondrial genome. *Nature*, **290**, 457–465.
2. Aquadro, C.F. and Greenberg, B.D. (1983). Human mitochondrial DNA variation and evolution: Analysis of nucleotide sequences from seven individuals. *Genetics*, **103**, 287–312.
3. Bamshad, M., Fraley, A.E., Crawford, M.H., Cann, R.L., Busi, B.R., Naudi and Jorde, L.B. (1996). mtDNA variation in caste populations of Andhra Pradesh, India. *Human Biology*, **68**, 1–28.
4. Barnabas, S., Apte, R.V. and Suresh, C.G. (1996a). Human evolution: the study of Indian mitochondrial DNA. *Naturwissenschaften*, **83**, 28–29.
5. Barnabas, S., Apte, R.V. and Suresh, C.G. (1996b). Ancestry and interrelationships of the Indians and their relationship with other world populations: A study based on mitochondrial DNA polymorphisms. *Ann. Hum. Genet.* (in press).
6. Batzer, M.A., Kilroy, G.E., Richard, P.E., Shaikh, T.H., Desselle, T.D., Hoppens, C.L. and Deininger, P.L. (1990). Structure and variability of recently inserted Alu family members. *Nuc. Acids. Res.* **18**, 6793–6798.
7. Batzer, M.A., Arcot, S.S., Phenny, J.W., Alegriahtortman, M., Kass, D.H., Milligan, S.M., Kimpton, C., Gill, P., Hochmeister, M., Ioannou, P.A., Herrera, R.J., Boudreau, D.A., Scheer, W.D., Keats, B.J.B., Deininger, P.L. and Stoneking, M. (1996). Genetic variation of recent Alu insertions in human populations. *J. Mol. Evol.* **42**, 22–29.
8. Bertranpetit, J., Sala, J., Calafell, F., Underhill, P.A., Moral, P. and Comas, D. (1995). Human mitochondrial DNA variation and the origin of Basques. *Ann. Hum. Genet.* **59**, 63–81.
9. Bhasin, M.K., Walter, H. and Danker-Hopfe, H. (1994). *People of India: An investigation of biological variability in ecological, ethno-economic and linguistic groups*. 41. Kamla-Raj Enterprises, Delhi.
10. Bonne-Tamir, B., Johnson, M.J., Natali, A., Wallace, D.C. and Cavalli-Sforza, L.L. (1986). Human mitochondrial DNA types in two Israeli populations—a comparative study at the DNA level. *Am. J. Hum. Genet.* **38**, 341–351.
11. Brega, A., Gardelk, R., Semino, O., Morpurgo, G., Ricatti, A., Wallace, D.C. and Santachiara Benerecetti, A.S. (1986). Genetic studies on the Tharu population of Nepal: Restriction endonuclease polymorphisms of mitochondrial DNA. *Am. J. Hum. Genet.* **39**, 502–512.
12. Brown, W.M. (1980). Polymorphism in mitochondrial DNA of humans as revealed by restriction endonuclease analysis. *Proc. Natl. Acad. Sci. USA*, **77**, 3605–3609.
13. Brown, W.M., George, M., Jr. and Wilson, A.C. (1979). Rapid evolution of animal mitochondrial DNA. *Proc. Natl. Acad. Sci. USA*, **76**, 1967–1971.
14. Brown, W.M. and Goodman, H.M. (1979). Quantitation of intrapopulation variation by restriction endonuclease analysis of human mitochondrial DNA. In *Extrachromosomal*

- DNA (D.J. Cummings, P.Borst, I.B. Dawid, S.M. Weissman and C.F. Fox eds.). 485–499. Academic Press, New York.
15. Cann, R.L., Stoneking, M. and Wilson, A.C. (1987). Mitochondrial DNA and human evolution. *Nature*. **325**, 31–36.
 16. Cavalli-Sforza, L.L., Piazza, A., Menozzi, P. and Mountain, J.L. (1988). Reconstruction of human evolution: Bringing together genetic, archaeological, and linguistic data. *Proc. Natl. Acad. Sci. USA*. **85**, 6002–6006.
 17. Cavalli-Sforza, L.L., Minch, E. and Mountain, J.L. (1992). Coevolution of genes and languages revisited. *Proc. Natl. Acad. Sci. USA*. **89**, 5620–5624.
 18. Childe, V.G. (1926). *The Aryans: A study of Indo-European origins*. Alfred A. Knopf, Inc.
 19. Darlu, P. and Tassy, P. (1987). Disputed African origin of Human Populations. *Nature*. **329**, 111–112.
 20. Deka, R., Jin, L., Shriver, M.D., Yu, L.M., Decroo, S., Hundrieser, J., Bunker, C.H., Ferrel, R.E. and Chakraborty, R. (1995a). Population genetics of dinucleotide (dC – dA)_n.(dG – dT)_n polymorphisms in world populations. *Am. J. Hum. Genet.* **56**, 461–474.
 21. Deka, R., Shriver, M.D., Yu, L.M., Ferrel, R.E. and Chakraborty, R. (1995b). Intra- and inter-population diversity at short tandem repeat loci in diverse populations of the world. *Electrophoresis*. **9**, 1659–1664.
 22. Denaro, M., Blanc, H., Johnson, M.J., Chen, K.H., Wilmsen, E., Cavalli-Sforza, L.L. and Wallace, D.C. (1981). Ethnic variation in HpaI endonuclease cleavage patterns of human mitochondrial DNA. *Proc. Natl. Acad. Sci. USA*. **78**, 5768–5772.
 23. Felsenstein, J. (1993). *PHYLIP* (Phylogeny Interference Package) Version 3.5. University of Washington.
 24. Giles, R.E., Blanc, H., Cann, H.M. and Wallace, D.C. (1980). Maternal inheritance of human mitochondrial DNA. *Proc. Natl. Acad. Sci. USA*. **77**, 6715–6719.
 25. Goldman, N. and Barton, N.H. (1992). Genetics and geography. *Nature*. **357**, 440–441.
 26. Goldstein, D.B., Linares, A.R., Cavalli-Sforza, L.L. and Feldman, M.W. (1995). Genetic absolute dating based on microsatellites and the origin of modern humans. *Proc. Natl. Acad. Sci. USA*. **92**, 6723–6727.
 27. Hammer, M.F. (1995). A recent common ancestry for human Y chromosome. *Nature*. **378**, 376–378.
 28. Horai, S., Hayasaka, K., Kondo, R., Tsugane, K. and Takahata, N. (1995). Recent African origin of modern humans revealed by complete sequences of hominoid mitochondrial DNAs. *Proc. Natl. Acad. Sci. USA*. **92**, 532–536.
 29. Hwu, H.R., Roberts, J.W., Davidson, E.H. and Britten, R.J. (1986). Insertion and/or deletion of many repeated DNA sequences in human and higher ape evolution. *Proc. Natl. Acad. Sci. USA*. **83**, 3875–3879.
 30. Johnson, M.J., Wallace, D.C., Ferris, S.D., Rattazzi, M.C. and Cavalli-Sforza, L.L. (1983). Radiation of human mitochondrial DNA types analyzed by restriction endonuclease cleavage patterns. *J. Mol. Evol.* **19**, 255–271.
 31. Jurka, J. (1993). A new subfamily of recently transposed human Alu repeats. *Nuc. Acids Res.* **21**, 2252.
 32. Jurkaka, J. and Zuckerandl, E. (1991). Free left arms as precursor molecules in the evolution of Alu sequences. *J. Mol. Evol.* **33**, 49–56.
 33. Kennedy, K.A.R., Sonakia, A., Chiment, J. and Verma, K.K. (1991). Is the Narmada Hominoid an Indian *Homo erectus*? *Am. J. Phys. Anthrop.* **86**, 475–496.
 34. Matera, A.G., Hillmann, U. and Schmid, C.W. (1990). A transcriptionally and transcriptionally competent Alu subfamily. *Mol. Cell. Biol.* **10**, 5424–5432.

35. Merriwether, D.A., Clark, A.G., Ballinger, S.W., Schurr, T.G., Soodyall, H., Jenkins, T., Sherry, S.T. and Wallace, D.C. (1991). The structure of human mitochondrial DNA variation. *J. Mol. Evol.* **33**, 543–555.
36. Mishra, S., Venkatesan, T.R., Somayajulu, B.L.K. and Rajguru, S.N. (1995). The earliest Acheulian Industry from peninsular India. *Current Anthropology*. **36**, 849–851.
37. Misra, V.N. (1989). Stone Age India: An ecological perspective. *Man and Environment*. **XIV**, (1), 17–64.
38. Mountain, J.L., Hebert, J.M., Bhattacharyya, S., Underhill, P.A., Ottolenghi, C., Gadgil, M. and Cavalli-Sforza, L.L. (1995). Demographic history of India and mtDNA-sequence diversity. *Am. J. Hum. Genet.* **56**, 979–992.
39. Nei, M. (1973). Analysis of gene diversity in subdivided populations. *Proc. Natl. Acad. Sci. USA*. **70**, 3321–3323.
40. Nei, M. (1985). Human evolution at the molecular level in Population Genetics and Molecular Evolution (T. Ohta and K. Aoki, eds.). *Japan Sci. Soc. Press*. Tokyo/Springer-Verlag, Berlin. 41–64.
41. Nei, M. and Li, W.H. (1979). Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proc. Natl. Acad. Sci. USA*. **76**, 5269–5273.
42. Nei, M. and Tajima, F. (1983). Maximum likelihood estimation of the number of nucleotide substitutions from restriction sites data. *Genetics*. **105**, 207–217.
43. Poloni, E.S., Excoffier, L., Mountain, J.L., Langaney, A. and Cavalli-Sforza, L.L. (1995). Nuclear DNA polymorphisms in a Mandenka population from Senegal: Comparison with eight other human populations. *Ann. Hum. Genet.* **59**, 43–61.
44. Renfrew, C. (1989). The origins of Indo-European languages. *Sci. Am.*, **261**, (4), 82–90.
45. Renfrew, C. (1994). World linguistic diversity. *Sci. Am.* **270**, (1), 104–110.
46. Rienzo, A.D. and Wilson, A.C. (1991). Branching pattern in the evolutionary tree for human mitochondrial DNA. *Proc. Natl. Acad. Sci. USA*. **88**, 1597–1601.
47. Rinehart, F.P., Ritch, T.G., Deininger, P.L. and Schmid, C.W. (1981). Renaturation rate studies of a single family of interspersed repeated sequences in human deoxyribonucleic acid. *Biochemistry*, **20**, 3003–3010.
48. Rogers, A.R. and Jorde, L.B. (1995). Genetic evidence of modern human origins. *Hum. Biol.* **67**, 1–36.
49. Santachiara Benerecetti, A.S., Scozzari, R., Semino, O., Torroni, A., Brega, A. and Wallace, D.C. (1988). Mitochondrial DNA polymorphisms in Italy. II Molecular analysis of new and rare morphs from Sardinia and Rome. *Ann. Hum. Genet.* **52**, 39–56.
50. Semino, O., Torroni, A., Scozzari, R., Brega, A. and Santachiara Benerecetti, A.S. (1991). Mitochondrial DNA polymorphisms among Hindus: A comparison with Tharus of Nepal. *Ann. Hum. Genet.* **55**, 123–136.
51. Singh, K.S. (1993). People of India: The profile of a national project (1985–92). *Curr. Sci.* **64**, 5–10.
52. Singh, K.S., Bhalla, V. and Kaul, L. (1994). *People of India, National series*. Anthropological Survey of India. Oxford University Press. **10**, 3.
53. Soodyall, H. and Jenkins, T. (1992). Mitochondrial DNA studies in the South African Indian population. *Gene Geogr.* **6**, (3), 127–137.
54. Templeton, A.R. (1991). Human origins and analysis of mitochondrial DNA sequences. *Science*. **255**, 737–739.
55. Tishkoff, S.A., Dietzsch, E., Speed, W., Pakstis, A.J., Kidd, J.R., Cheung, K., Bonne-Tamir, B., Santachiara-Benerecetti, A.S., Moral, P., Krings, M., Paabo, S., Watson, E., Risch, N., Jenkins, T. and Kidd, K.K. (1996). Global patterns of linkage disequilibrium at the CD4 locus and modern human origins. *Science*. **271**, 1380–1387.

56. Throne, A.G. and Wolpoff, M.H. (1992). The multiregional evolution of humans. *Sci. Am.* **266**, (4), 28–33.
57. Ullu, E. and Tschudi, C. (1984). Alu sequences are processed 7SL RNA genes. *Nature*. **312**, 171–172.
58. Vawter, L. and Brown, W.M. (1986). Nuclear and mitochondrial DNA comparisons reveal extreme rate variation in the molecular clock. *Science*. **234**, 194–196.
59. Vigilant, L., Stoneking, M., Harpending, H., Hawkes, K. and Wilson, A.C. (1991). African populations and the evolution of human mitochondrial DNA. *Science*. **253**, 1503–1507.
60. Wainscoat, J.S., Hill, A.V.S., Boyce, A.L., Flint, J., Hernandez, M., Thein, S.L., Old, J.M., Lynch, J.R., Falusi, A.G., Weatherall, D.J. and Clegg, J.B. (1986). Evolutionary relationships of human populations from an analysis of nuclear DNA polymorphisms. *Nature*. **319**, 491–493.
61. Wallace, M.R., Anderson, L.B., Saulino, A.M., Gregory, P.E., Glover, T.W. and Collins, F.S. (1991). A de novo Alu insertion results in neurofibromatosis type 1. *Nature*. **353**, 854–866.
62. Weiner, A.M., Deininger, P.L. and Efstratiadis, A. (1986). Nonviral retroposons: genes, pseudogenes and transposable elements generated by the reverse flow of genetic information. *Ann. Rev. Biochem.* **55**, 631–661.
63. Whitefield, L.S., Loveli-Badge, R. and Goodfellow, P.N. (1993). Rapid sequence evolution of the mammalian sex-determining gene SRY. *Nature*. **364**, 713–715.
64. Wilson, A.C. and Cann, R.L. (1992). The recent African genesis of humans. *Sci. Am.* **266**, (4), 22–27.

People of India: Biological diversity and affinities

Partha P. Majumder

Anthropology and Human Genetics Unit, Indian Statistical Institute, Calcutta

Introduction

The Indian subcontinent comprises a vast collection of peoples with different morphological, genetic, cultural and linguistic characteristics. While much of this variability is indigenous, a considerable fraction of this variability has been introduced through large-scale immigrations into India during historical times. From an evolutionary standpoint, it is of immense interest to quantify biological diversity in contemporary human populations, to study biological affinities and to relate observed patterns of affinities with cultural, linguistic and demographic histories of populations. Such efforts are intended to shed light on our biological heritage and on the peopling of India.

Physical anthropologists have been engaged in systematically studying physical characteristics of the Indian peoples from about the turn of this century. The data collected in these early studies provided ample evidence of enormous anthropometric variation among different Indian populations. The overt goal of most of these studies conducted until about 1950 was typological—to classify the peoples of India into a number of ‘racial’ types [Risley, 1908; Eickstedt, 1934; Guha, 1935; Sarkar, 1954]. Over the course of the next few decades, such typological studies increasingly fell out of favour, and physical anthropologists turned their attention to specific regions—e.g. Uttar Pradesh [Mahalanobis et al., 1949], Gujarat [Majumdar and Sen, 1949], Maharashtra [Majumdar and Rao, 1960], Bengal [Malhotra, 1978]—quantifying variability and studying relationships. The availability of blood grouping techniques and subsequently electrophoretic techniques provided additional repertoire for the conduct of such studies.

The purpose of this paper is to present a very broad overview of the physical (anthropometric) and genetic diversities and affinities of the peoples of India. We shall also attempt to examine how well biological—in particular, genetic—diversities and affinities correlate with geographical, socio-cultural and linguistic diversities and affinities.

The paradigm

It may not be inappropriate to make a few remarks about the paradigm underlying the reconstruction of peopling of a geographical area. The short-term paradigm is depicted

in Fig. 1. With the passage of time, there is fission of populations into subpopulations. Such fissions occur because of various cultural and demographic reasons. The consequent demographic impact, primarily population size bottle-necks, result in increase in genetic diversity among subpopulations because of genetic drift. When such subpopulations remain isolated from one another, i.e., individuals of one subpopulation do not exchange mates with other subpopulations, genetic diversification is hastened. (Fusion of populations also occurs, but is much less common than fission.) Admixture (exchange of genes) between subpopulations increases genetic affinities. The primary forces that are barriers to admixture are cultural and linguistic differences and geographical distance. Thus, one expects genes, cultures and languages to evolve in tandem, especially for such genes that are not subjected to differential pressures of natural selection. It is because of this expected phenomenon that correlating genetic diversities and affinities with cultural and linguistic histories is of potential interest to human biologists. In general, the longer two populations are separated, the larger is the genetic distance between them. Genetic distance, therefore, is a useful clock by which to date evolutionary history.

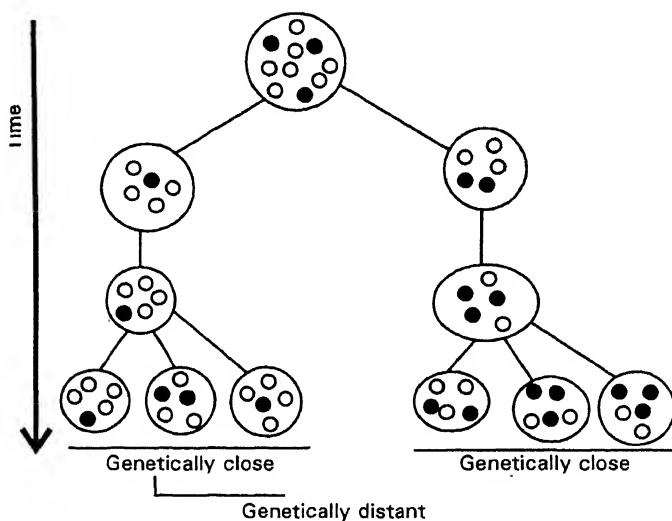


Fig. 1 *The evolutionary paradigm of genetic studies of contemporary human populations*

People of India: Some broad characteristics

Morphologically, the people of India may be broadly classified [Malhotra, 1978] into four types—Negrito, Australoid, Mongoloid and Caucasoid. The characteristics and present geographical distributions of these types are provided in Table 1. Population groups belonging to the Hindu caste structure are hierarchically organised in Upper, Middle and Lower strata. Cultural norms act as barriers to inter-caste marriage, particularly when the castes in question do not belong to the same hierarchical rung.

One therefore expects caste groups belonging to the same rung to be biologically 'closer' than groups belonging to different rungs. Tribal groups do not have a uniform religion; many are ancestor worshippers. Many groups, e.g., Muslim, Christian and Sikh, do not belong to the Hindu or the tribal fold; these groups are also maritally closed. However, even within such groups there are often barriers to free intermarriage because of the existence of sects. Linguistically, the non-tribal groups of northern India are Indo-European and those of southern India are Dravidian. The tribal groups belong to one of four broad linguistic families—Austro-Asiatic (Khasi, Santhali, Ho, Mundari, Gondi, etc.), Tibeto-Burman (Bhotia, Lepcha, Miri, Kachari, Angami, Lushai, etc.), Dravidian (Korwa, Yerukula, etc.) and Indo-European (Hajong, Bhili, etc.).

Table 1 *Morphological types, features and present geographical distribution of the people of India*

Type	Morphological Characterisation	Present Distribution
Negrito	Short stature, frizzly hair, fine hair texture, brachycephalic head, dark complexion, short and protruding face, broad nose, thick and everted lips.	Andaman Islands, Nilgiri Hills of Tamil Nadu. May have had a wide distribution at one time.
Australoid	Short stature (taller than Negrito), wavy to curly hair, hyperdolichocephalic to dolichocephalic head, dark complexion, stout brow ridges, sunken nasal root, abundance of body hair.	Chiefly in central and southern regions.
Mongoloid	Short stature, broad shoulder, scanty facial and body hair, brachycephalic head, flat face, prominent cheek bones, flat nose, epicanthic fold.	Sub Himalayan and northeastern regions.
Caucasoid	Generally tall stature, dolichocephalic to brachycephalic head, light complexion, straight to wavy hair, sometimes light eyes, arched forehead, long face with well-developed chin, narrow and prominent nose.	Found in most regions.

Physical diversity and affinities in India

The shapes of head and nose are two of the key features that characterise physical types. These features are also known to be relatively less affected by the environment. Figure 2 provides mean values of cephalic index [= (Head Breadth/Head Length) × 100]

Figure 2 provides mean values of cephalic index [= (Head Breadth/Head Length) \times 100] and nasal index [= (Nose Breadth/Nose Length) \times 100] in various socio-cultural and geographical subsets of the Indian peoples. It is clear from this figure that there is considerable diversity in head and nose shapes among geographical regions and socio-cultural groups. It is also clear that a prominent discriminator of upper caste Brahmins from tribals is nose shape: the tribals have a characteristically broader nose.

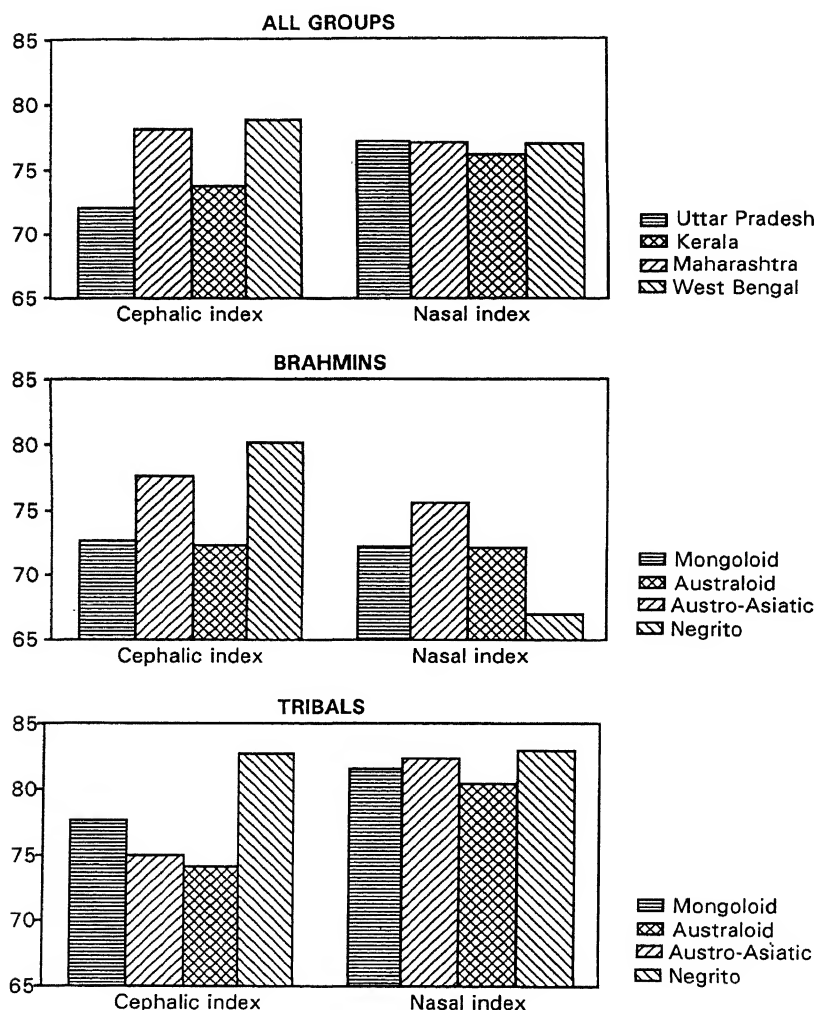


Fig. 2 Mean values of cephalic and nasal indices in pooled populations and upper caste Brahmins of four Indian states from four geographical regions (North: Uttar Pradesh; West: Maharashtra; South: Kerala; East: West Bengal) and tribal populations of various morphological types

To understand physical affinities among population groups of India, we had [Majumder et al., 1990] conducted a cluster-analytic study using data on 7 anthropometric characters of 82 populations from different geographical regions of India. This study revealed that the populations cannot be grouped into large clusters. The largest cluster that was identified in this study comprised the following populations: Agarwal (Uttar Pradesh, middle caste), Agharia (Uttar Pradesh, middle caste), Ahir (Delhi, middle caste), Baisya (West Bengal, middle caste), Chhatri (Uttar Pradesh, middle caste), Gujjar (Delhi, middle caste), Jat (Delhi, middle caste), Kaibarta (West Bengal, middle caste), Kamma (Andhra Pradesh, middle caste), Kayastha (West Bengal, middle caste), Kshatriya (West Bengal, middle caste), Kurmi (Uttar Pradesh, middle caste), Nav Buddha (Uttar Pradesh, lower caste), Panika (Uttar Pradesh, tribal Australoid), Pariah (Andhra Pradesh, low caste), Rajput (Uttar Pradesh and Delhi, middle caste) and Sankhari (West Bengal, middle caste). This cluster, therefore, includes populations from diverse geographical regions and diverse socio-cultural backgrounds. Even though our study [Majumder et al., 1990] revealed that there are statistically significant differences in physical characteristics of the Indian peoples inhabiting different geographical regions as well as having different ethnic backgrounds, the patterns of clustering of the populations clearly showed that these two factors are insufficient to explain the anthropometric variation observed at the all-India level. Because anthropometric characters are known to be affected by the environment, it is useful to verify such a conclusion using genetic data.

Genetic diversity and affinities in India

One measure of genetic diversity is what is termed as the average heterozygosity, H . (The average is taken over a large number of genetic loci, L . The heterozygosity at the l th locus ($l = 1, 2, \dots, L$), h_l , is defined as $1 - \sum_{i=1}^{n_l} p_i^2$, where p_i denotes the frequency of the i th allele at this locus with n_l alleles. h_l is a measure of the proportion of individuals in the population who are heterozygous at this locus). Genetic variation is greatly reduced in a heavily inbred population over generations. Variations in alleles, i.e., in genes representing alternative realisations of the same character such as the colour of the eyes, are minimised. Individuals here tend to carry identical alleles and are called homozygotic. With outbreeding and mixing, genetic diversity is introduced. Variations in the same genetic locus, e.g. alleles obtained here are termed as heterozygous. (See Chapter 3). Figure 3 provides values of average heterozygosity among Indians and three major global morphological groups—Caucasoids, Mongoloids and Negroids. It is seen that the extent of genetic diversity is comparable to or is even greater than some of the major morphological groups. To provide one concrete example of the extent of genetic variation among the peoples of India, we consider the MN blood group locus. At this locus, the M allele frequency varies from 0.35 (among Tamangs of Jalpaiguri district of West Bengal) to 0.90 (among Maria Gonds of Andhra Pradesh and Maharashtra).

There is extensive genetic diversity not only at the all-India level but also within smaller geographical regions of India. This is depicted in Fig. 4.

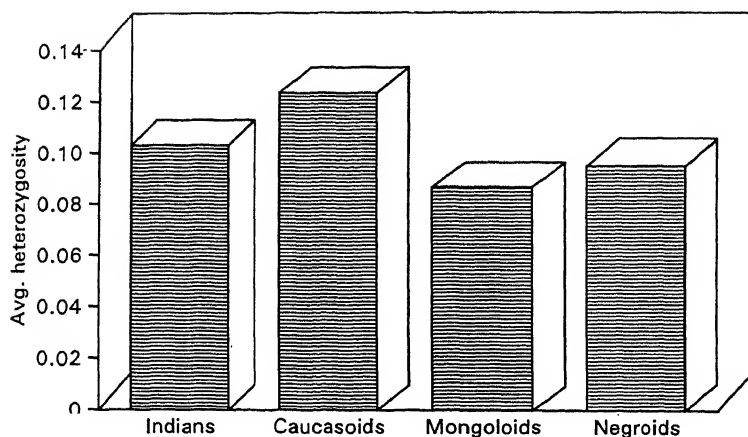


Fig. 3 Average heterozygosities based on data of 29 loci among Indians and global morphological groups

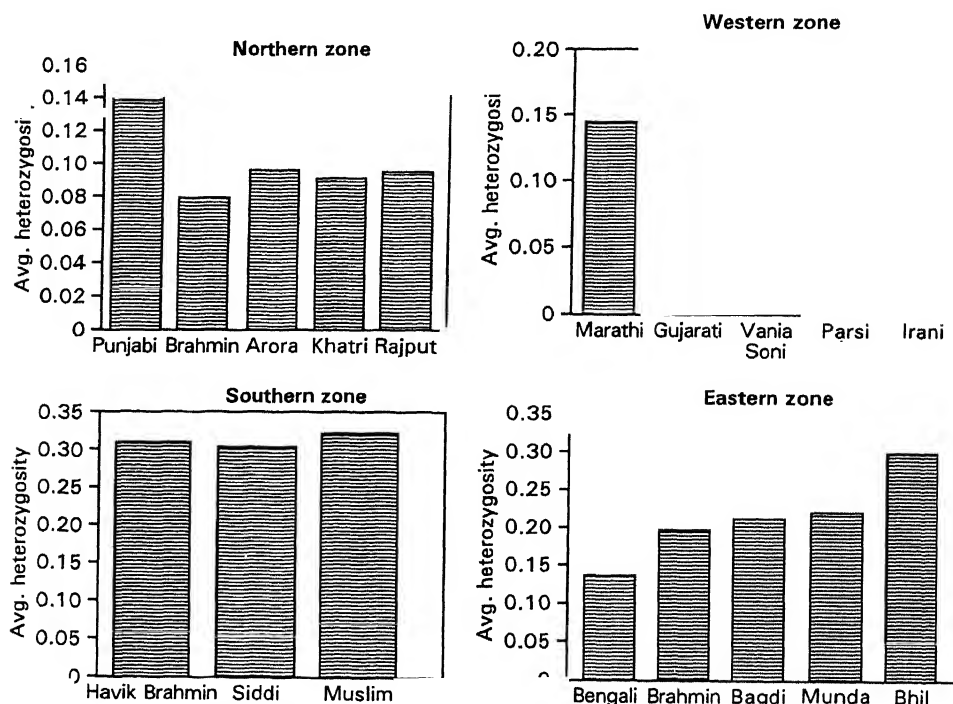


Fig. 4 Average heterozygosities based on data of a variable (10–21) number of loci, in some defined ethnic groups from four geographical regions of India

How are the Indians genetically positioned relative to Caucasoids, Mongoloids and Negroids? This question has been examined [Roychoudhury, 1977; Walter, 1971]; the genetic relationships (based on data of 29 loci) are depicted in Fig. 5. Roughly speaking, Indians are genetically equidistant from Caucasoids and Mongoloids, but quite distant from Negroids.

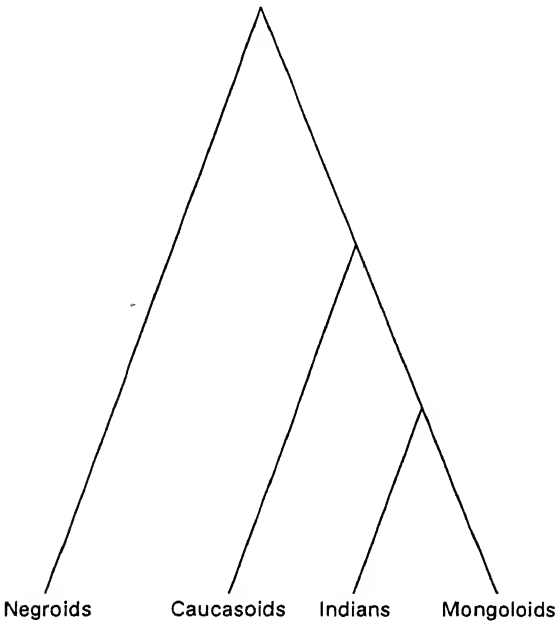


Fig. 5 Dendrogram depicting genetic affinities, based on data of 29 loci, among Indians and global morphological groups

How are populations from various Indian regions genetically positioned relative to one another? Using the data on allele frequencies at 10 loci presented by Roychoudhury (1977), a single-linkage dendrogram (Fig. 6) was constructed. From Fig. 6 it is seen that the populations of southern India stand apart genetically from the populations of North, West (Marathi, Gujarati), East (Bengali) and Central (Madhya Pradesh) India.

While the inferences presented above pertain to a very macrolevel, using anthropologically ill-defined groups (such as Indians, South Indians and so on), it is of interest to consider patterns of genetic affinities among endogamous groups inhabiting smaller geographical regions. The specific question to be answered is: within smaller geographical regions, are endogamous groups at the same level of socio-cultural hierarchy/affiliation genetically more close or are populations inhabiting geographically closer areas genetically closer irrespective of their socio-cultural affiliation? Put differently, does geographical distance between habitats have a stronger effect in determining genetic affinities than socio-cultural backgrounds? To examine this issue, we shall consider only two regions of India—eastern and southern.

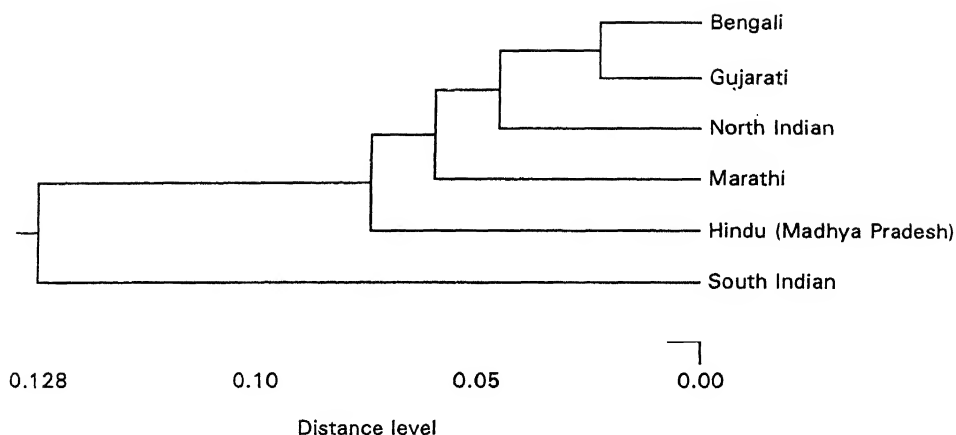


Fig. 6 Dendrogram depicting genetic affinities, based on data of 10 loci, among populations from different geographical regions of India. (Note: Bengalis are from eastern India, Gujaratis and Marathis are from western India, Hindus of Madhya Pradesh are from central India.)

Based on a genetic survey carried out primarily by the Indian Statistical Institute in the eastern Indian states of Bihar, Orissa, West Bengal, Assam and Manipur, we have attempted to investigate the genetic relationships of populations in this zone. Twenty-four population groups have been included in this analysis. These are—Bihar [Saha et al., 1992]: Brahmin (upper caste), Chamar (low caste), Santal (tribe), Bhuiya (tribe), Muslim; Orissa [Reddy et al., 1989]: Vadabaliya (low caste; subdivided into two isolates at Penticotta and Vadapeta), Jalari (low caste), Kevto (low caste); West Bengal [Banerjee et al., 1992]: Poliya, Deshi, Tiyyor (all low caste and descendants of the Koch); Assam [Walter, 1986]: Brahmin (upper caste), Kalita (middle caste), Kaibarta (low caste), Muslim Ahom (ancestral population of Assam; migrant from Myanmar), Karbi (tribe), Kachari (tribe), Sonowal (a division of Kachari), Rajbanshi (low caste), Chutiyas (ancestral population of Assam; tribe) [Mukherjee et al., 1989; Das et al., 1987]; Manipur [Singh et al., 1986]: Brahmin (upper caste), Meitei (middle caste). Based on gene frequency data of 5 loci—ABO, HP, ACP, ESD, AK—a dendrogram of genetic relationships was constructed (Fig. 7). Figure 7 indicates that, by and large, the genetic clustering of these populations is based on geographical contiguity of habitats. The two population samples from Manipur cluster together. The four population samples from Orissa also cluster together. The low caste (Chamar) and tribal groups (Bhuiya and Santal) of Bihar cluster together. The high caste Brahmins and Muslims of Bihar show close genetic affinity. In this context, it may be mentioned that Majumdar and Rao (1960) had also noted anthropometric similarities of the Muslims of some regions of Bengal with the higher castes, and concluded that the conversion of Hindus to Muslims (which is a historical fact) had taken place not only from the lower castes but also from the higher castes. It is unclear why the Brahmins and Muslims of Bihar show close genetic affinities with the Chutiyas of Assam. It is, however, noteworthy that the Chutiyas, who are an ancient

population of Assam, were subjugated by the migrant Ahoms and were pushed to their present localised territory in upper Assam. This may have resulted in certain peculiarities in their genetic profile which distinguishes them from the other populations of Assam. The three descendant populations of the Koch (who ruled vast areas of Assam and northern West Bengal until about 300 years ago)—Poliya, Deshi and Tiyor—show close genetic affinities among themselves and also with the Karbi of Assam. The genetic affinities among the population samples of Assam do not show any large degree of congruence with socio-cultural hierarchy.

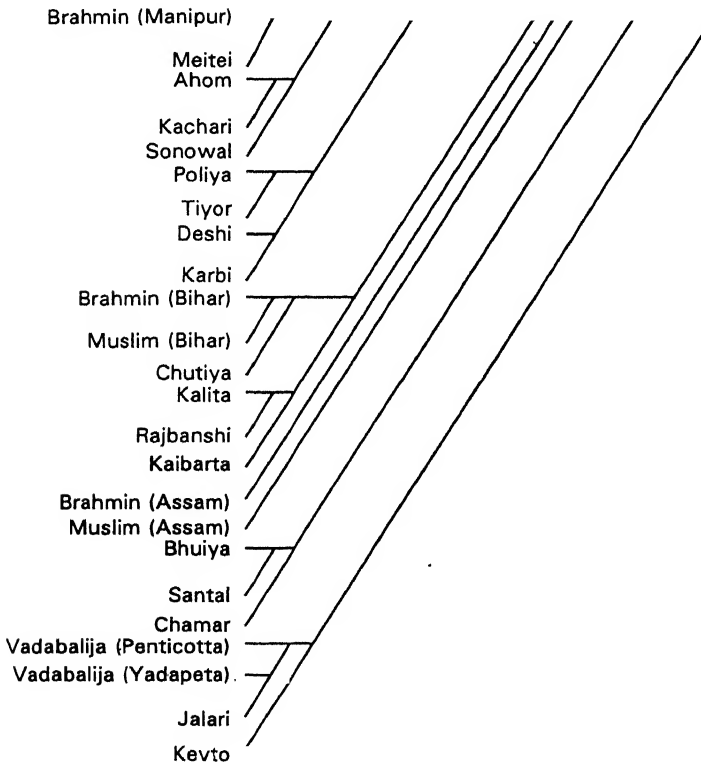


Fig. 7 Dendrogram depicting genetic affinities among populations of eastern India

The Indian Statistical Institute also conducted genetic surveys [Banerjee et al., 1988; Vijayakumar et al., 1987] among several endogamous groups of South India, including those of Andhra Pradesh, Karnataka, Tamil Nadu and Kerala. In this study we have analysed the data pertaining to A₁, A₂, BO, RH, ACP, ESD and HB loci of 16 populations. The populations included from the various States are—Andhra Pradesh: Vaidik Brahmin (upper caste), Vysya (middle caste), Kamma (middle caste); Karnataka: Lingayat (upper caste), Vokkaliga (middle caste), Jenu Kuruba (tribe), Siddi (subdivided into three religious isolates—Hindu, Muslim and Christian; brought into India

as slaves primarily from east Africa; Negroid); Tamil Nadu: Chettiar (middle caste), Pariah (low caste), Kallan (low caste); Kerala: Namboodiri Brahmin (upper caste), Ezhava (middle caste), Pulayan (low caste), Urali (tribe). Except for the Siddis, all the other groups speak Dravidian languages. The Siddis are multi-lingual and speak both Indo-European and Dravidian languages.

Figure 8 depicts the genetic relationships among these 16 populations, from which it is clear that the Siddis are genetically distinct from the other South Indian populations. This is expected because the Siddis are immigrants into India from Africa; they have retained their genetic identity because of restricted admixture with indigenous populations of southern India. Figure 8 also shows that there is no correspondence between genetic and socio-cultural affinities. In fact, there are indications, albeit weak, that genetic similarity in this zone decreases with increase in geographical distance.

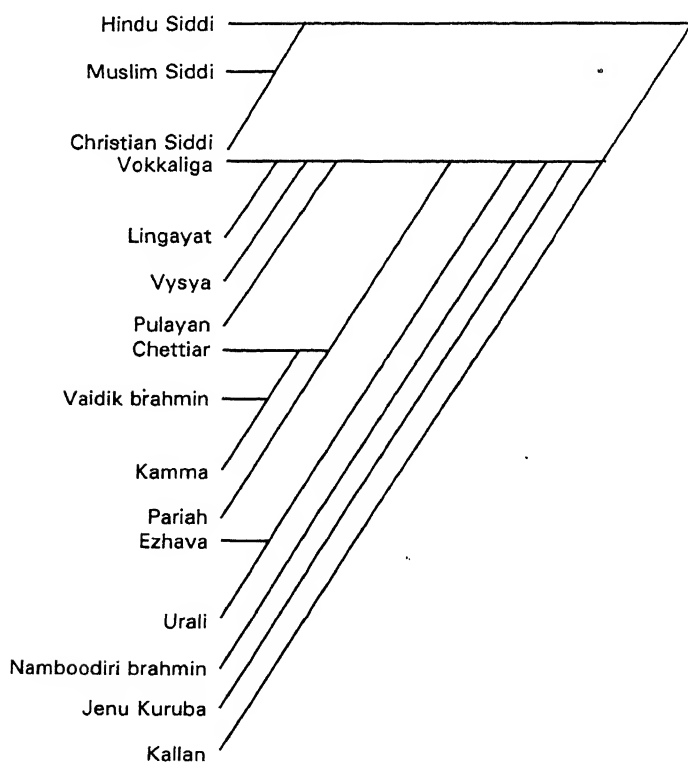


Fig. 8 *Dendrogram depicting genetic affinities among populations of southern India*

The overall inference from the data presented above is that, in both eastern and southern regions of India, geographical proximity has a stronger effect than socio-cultural proximity in determining genetic affinity. Similar patterns are observed in northern, western and central India [Majumder and Mukherjee, 1993; Das et al., 1996] and also within smaller geographical areas [Majumder and Mukherjee, 1993; Papiha et al., 1996].

Can geographical clines of allele frequencies be identified?

Since geographical distance seems to be a determinant, although somewhat weak, of genetic distance between populations of India, it is of interest to investigate whether geographical clines can be identified in respect of allele frequencies at any locus. Because data on A, B and O bloodgroup allele frequencies are the most extensive, we have conducted a spatial auto-correlation analysis [Mukherjee and Majumder, 1995] of these data. In this analysis, a total of 830 datasets of diverse caste and tribal populations from across India were included. The results are graphically presented in Fig. 9. It is seen that spatial auto-correlation (as measured by Moran's I statistic) is significant only in respect of the A allele among caste populations at a distance class of 2 (distance classes of 1 degree latitude and 1 degree longitude were formed in this analysis). This implies that the spatial distributions of A, B and O allele frequencies on the Indian subcontinent are very patchy. Even when the spatial auto-correlation for the A allele frequency among caste groups was found to be significant, no clear geographical cline could be discerned at the all-India level.

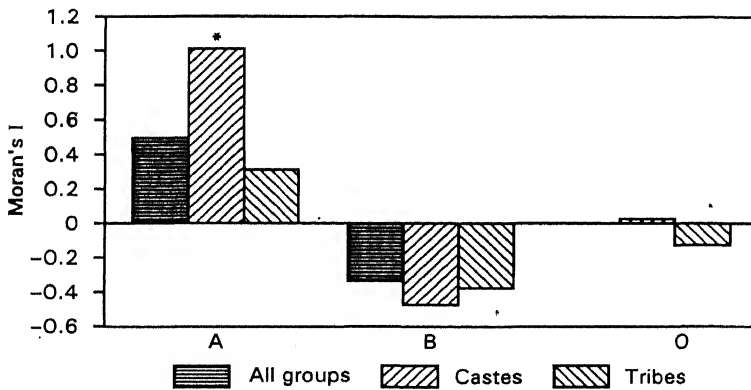


Fig. 9 Results of spatial auto-correlation analysis of A, B and O allele frequencies on Indian subcontinent separately for all (irrespective of socio-cultural affiliation) population groups, caste groups and tribal groups. (Note: Asterisk indicates that Moran's I is statistically significant at the 5% level for A allele frequency among caste groups.)

How well do patterns of biological affinities correlate with cultural history of India?

The major findings of our study of physical and genetic diversities and affinities among Indian populations are: (i) Indian populations harbour more genetic diversity than populations of comparable geographical regions; (ii) Indians genetically are between Caucasoids and Mongoloids; (iii) southern and northern Indians are genetically quite distinct; (iv) geographical contiguity of habitat, rather than socio-cultural affiliation,

plays a more significant role in determining physical and genetic affinities among Indian populations; and (v) the spatial profiles of allele frequency surfaces, in respect of the ABO blood group locus, are very patchy. Since cultural factors play an important role in determining gene flow between populations and, consequently, in determining patterns of biological affinities, it is pertinent to examine biological findings in the light of socio-cultural history. It is known that the structure of the contemporary Indian society is quite complex with groups at widely different socio-cultural and economic levels co-existing, often in close proximity to one another. We briefly recall the history of India with specific reference to population movements in order to understand the complex character of the contemporary Indian society and, in turn, to meaningfully interpret our biological findings. Traces of human activity can be found in India sometime between 400,000–200,000 BC. Neolithic settlements are evident around this period, and it appears beyond doubt [Rapson, 1955] that Austric languages are descended from the neolithic peoples. The Indus Valley Civilisation, which began around 300 BC and lasted for about 1500 years, saw flourishing trade contacts with the Persian Gulf and Mesopotamia. Although there is considerable debate [Rapson, 1955; Allchin and Allchin, 1982] whether Dravidian languages owe their origin to neolithic peoples of southern India or whether they were brought into India, there is evidence that Dravidian speakers, who included settled agriculturists, predominated both northern and southern India. During the period 1500 BC to about AD 11, northwestern and northern India turned into a melting pot. The year 1500 BC saw the entry of Indo-Aryan speakers from Bactria and Iran. Their entry witnessed the beginning of a long period of conflicts and conquest of indigenous peoples. Caste system was formed soon after the entry of the Indo-Aryan speakers. During the period 800–500 BC, iron was introduced, which provided the means for large-scale expansion of the Indo-Aryan speakers into the Gangetic valley. Linguistic imperialism was firmly established resulting in the submergence of Austric languages. There was a large-scale recedence of indigenous peoples of the north to farther and farther south. The period from 520 BC to AD 300 witnessed successive invasions by Persians, Greeks and Scythians. This was followed by invasions by Central Asian nomadic tribals (Huns), Arabs and Turks until AD 1100. Thus, not only were there large-scale movements of peoples (invaders) with diverse genetic backgrounds into India, their entry also resulted in trade contacts with China and Southeast Asia. The northeast of India also witnessed conquests, e.g., the conquest of Kamarupa (Assam) by Ahoms, a Shan people, in AD 1253. During this long period of turbulence and establishment of cultural contacts in northern India, southern India, by and large, developed independently. However, maritime trade links also developed; during 200 BC–AD 300, Roman and Southeast Asian trade flourished; during AD 300–700, trade with the east African coast peaked; during AD 700–1300, flourishing trade continued with Arabs and the Semitic people. Most of these early trade settlements were confined to the port areas of coastal India, particularly in southern India. In more recent times, traders from various parts of the world arrived in India—Portuguese (late 1550s), Dutch (early 1700s), English (1610), French (1725).

Since genes move with people, the entry of diverse genetic elements into India must be a major reason for the extraordinary biological diversity of contemporary Indian

peoples. The fact that Dravidian-speaking southern India remained relatively sheltered from the Indo-Aryan influence is probably the major reason why south Indian populations are genetically distinct from north Indian populations. The Indo-Aryan speakers, who entered through northwestern and western corridors, diffused in all directions, receiving a check only in the south where Dravidian languages were firmly established. In other words, there was relatively little admixture of diverse genetic elements with indigenous genetic stocks in southern India compared to northern India.

In spite of the linguistic homogeneity in southern India, the cultural barriers relating to free intermarriage created by the caste system has probably been a major reason for genetic diversification among the people of this region. The lack of appropriate means of transport to cross geographical barriers further accentuated genetic diversification between populations.

Northern India, as stated above, has been a genetic melting pot. Here, as in southern India, we see that the genetic affinities do not correlate with socio-cultural affiliation, but with geographical proximity. In particular, there has been large-scale conversion of Hindus to Islam. These conversions may not have been restricted to people belonging to lower castes, which is why Muslims of different areas of north India show close genetic affinities with caste groups at different levels of hierarchy.

If one were to make a general statement regarding the pattern of genetic affinities vis-a-vis cultural and geographical affinities among population groups of India, the one major feature that has emerged is that geographical affinity plays a stronger role than cultural affinity in determining genetic affinity. This seems somewhat counter-intuitive from an anthropological viewpoint, particularly because of the strong restrictions imposed on free intermarriage by the cultural traditions of the country. Even though these restrictions continue to have a significant impact on who marries whom in India, it is clear from population genetics theory [Slatkin, 1985] that the process of genetic homogenisation of two genetically disparate populations does not require a great amount of admixture between the populations over a long period of time. (The rate of homogenisation is primarily dependent on the extent of initial differences in allele frequencies between the two populations, their effective population sizes and the admixture rate per generation between them.) Therefore, even when two culturally distinct populations are classified by an anthropologist as two distinct endogamous groups because of a 'low' rate of admixture between them (say, < 0.01% of all marriages per generation), in terms of genetic homogenisation this rate may be very high. In other words, the fact that cultural affinity does not play as strong a role in determining genetic affinity between populations may not really be very counter-intuitive. Geographical distance of habitat, irrespective of cultural affinity, may indeed be the limiting factor for flow of genes between populations in India, which is perhaps why geographical proximity is found to be a stronger determinant of genetic affinity.

The road ahead

As seen from the foregoing discussion, the study of genetic diversity on the Indian subcontinent during the past several decades has provided valuable insights into the

genetic structures and affinities among Indian populations. However, because of the inherent limitations of serological and biochemical genetic markers, it has not been possible to trace genetic trails of historical migrations or even to reconstruct the peopling of the subcontinent to any good degree of satisfaction. More importantly, because such studies lacked coordination, the data generated have proved to be of limited value. In more than 60% of the 2000 (approx.) populations investigated to date, only one locus (primarily the ABO blood group locus) has been screened. The number of populations in which more than 5 loci were screened is only about 15%. Even among studies in which more than 5 loci were screened, the sets of loci screened were often disjoint. Thus, one is left with no choice but to either pool anthropologically well-defined populations with ill-defined ones (e.g., Bengali, south Indian, etc.) to increase the number of common loci for purposes of statistical analyses, or to retain well-defined group identities and use data on a reduced number of loci; both options are unwelcome for population genetic purposes. Recent advances in molecular genetics permit the choice of highly heterozygous markers and markers that are linked (permitting haplotype construction). Therefore, potentially much more informative markers can now be screened in human population genetic studies. Such markers need to be judiciously chosen and, more importantly, such studies in the future need to be coordinated in order that a minimum number of core loci are screened in every study to ensure a minimum degree of data comparability. We hope such studies on the diversity among Indian populations will continue, that a more informative battery of genomic markers will be used and that future studies will be conducted in a coordinated manner in order that we can not only reconstruct human evolution in India but also construct a database useful for the study of genetic epidemiology of various diseases in India.

References

1. Allchin, B. and Allchin, R. (1982). *The Rise of Civilization in India and Pakistan*. Cambridge University Press, Cambridge.
2. Banerjee, S., Roy, M., Dey, B., Mukherjee, B.N. and Bhattacharjee, S.K. (1988). Genetic polymorphism of red cell antigen, enzyme, haemoglobin and serum protein in fifteen endogamous groups of south India. *Jour. Indian Anthropol. Soc.* **23**, 250–262.
3. Banerjee, S., Das, M.K., Das, K., Dey, B., Roy, M. and Mukherjee, B.N. (1992). Genetic differentiation among the three Hindu low caste groups of Malda District, West Bengal, India. *Internat. Jour. Anthropol.* **7**, 7–17.
4. Das, B.M., Walter, H., Gilbert, K., Lindenberg, P., Malhotra, K.C., Mukherjee, B.N., Deka, R. and Chakraborty, R. (1987). Genetic variation of five blood group polymorphisms in ten populations of Assam, India. *Internat. Jour. Anthropol.* **2**, 325–334.
5. Das, K., Malhotra, K.C., Mukherjee, B.N., Walter, H., Majumder, P.P. and Papiha, S.S. (1996). Population structure and genetic differentiation among 16 tribal populations of central India. *Hum. Biol.* **68**, 679–705.
6. Guha, B. S. (1935). The racial affinities of the people of India. In *Census of India, 1931*. I. India, Pt. 3A, 2–22. Delhi, Government of India Press.
7. Mahalanobis, P.C., Majumdar, D.N. and Rao, C.R. (1949). Anthropometric survey of the United Provinces, 1941: A statistical study. *Sankhya*. **9**, 90–324.

8. Majumdar, D.N. and Rao, C.R. (1960). *Race Elements in Bengal: A Quantitative Study*. Calcutta, Asia Publishing House and Statistical Publishing Society.
9. Majumdar, D.N. and Sen, A.R. (1949). Anthropometric status of castes and tribes. In *Race Realities of Cultural Gujarat*. Gujarat Cultural Society. 22–64.
10. Majumder, P.P., Uma Shankar, B., Basu, A., Malhotra, K.C., Gupta, R., Mukhopadhyay, B., Vijayakumar, M. and Roy, S.K. (1990). Anthropometric variation in India: A statistical appraisal. *Curr. Anthropol.* **31**, 94–103.
11. Majumder, P.P. and Mukherjee, B.N. (1993). Genetic diversity and affinities among Indian populations: An overview. In P.P. Majumder ed. *Human Population Genetics: A Centennial Tribute to J.B.S. Haldane*. New York, Plenum Press. 255–275.
12. Malhotra, K.C. (1978). Morphological composition of the people of India. *J. Hum. Evol.* **7**, 45–63.
13. Mukherjee, B.N., Malhotra, K.C., Roy, M., Banerjee, S., Walter, H. and Chakraborty, R. (1989). Genetic heterogeneity and population structure in eastern India: Red cell enzyme variability in ten Assamese populations. *Z. Morph. Anthropol.* **77**, 287–299.
14. Mukherjee, B.N. and Majumder, P.P. (1995). Spatial auto-correlation analysis reveals that A,B and O allele frequency surfaces on the Indian subcontinent are highly fractured. *Z. Morph. Anthropol.* **81**, 33–39.
15. Papiha, S.S., Chahal, S.M.S. and Mastana, S.S. (1996). Variability of genetic markers in Himachal Pradesh, India: Variation among subpopulations. *Hum. Biol.* **68**, 629–654.
16. Rapson, E.J. (1955). Peoples and languages. In E.J. Rapson ed. *Cambridge History of India: Ancient India*. S. Chand and Co., Delhi. **1**, 33–57.
17. Reddy, B.M., Chopra, V.P., Rodewald, A., Mukherjee, B.N. and Malhotra, K.C. (1989). Genetic differentiation among four groups of fishermen of the eastern coast, India. *Ann. Hum. Biol.* **16**, 321–326.
18. Risley, H.H. (1908). *People of India*. Thacker Spink & Co., Calcutta.
19. Roychoudhury, A.K. (1977). Genetic diversity in Indian populations. *Hum. Genet.* **40**, 99–106.
20. Saha, N., Tay, J.S.H., Roy, A.C., Das, M.K., Das, K., Roy, M., Dey, B., Banerjee, S. and Mukherjee, B.N. (1992). Genetic study of five populations of Bihar, India. *Hum. Biol.* **64**, 175–181.
21. Sarkar, S.S. (1954). *The Aboriginal Races of India*. Bookland, Calcutta.
22. Singh, K.S., Mukherjee, B.N., Walter, H., Lindenberg, P., Gilbert, K., Dannewitz, A., Malhotra, K.C., Banerjee, S., Roy, M. and Dey, B. (1986). Genetic markers among Meiteis and Brahmins of Manipur, India. *Hum. Hered.* **36**, 177–184.
23. Slatkin, M. (1985). Gene flow in natural populations. *Ann. Rev. Ecol. Sys.* **16**, 53–65.
24. Vijayakumar, M., Malhotra, K.C., Walter, H., Gilbert, K., Lindenberg, P., Dannewitz, A., Sorensen, A., Chakraborty, R., Reddy, A.P. and Mukherjee, B.N. (1987). Genetic studies among Siddis of Karnataka, India: A migrant population from Africa. *Anthropol. Anz.* **77**, 92–107.
25. Von Eickstedt, E. (1934). *Rassenkunde und Rassengeschichte der Menschheit*. Stuttgart, Ferdinand Euke Verlag.
26. Walter, H. (1971). Notes on the distribution of serum protein polymorphism in India. In M.R. Chakravarti ed. *Proceedings of the International Symposium on Human Genetics*. Andhra University Press, Waltair. 205–216.
27. Walter, H. (1986). Genetic differentiation processes among the populations of India. *Internat. Jour. Anthropol.* **1**, 297–308.

Contribution of geochronology to Indian human heritage

S. Mishra, S.N. Rajaguru
Deccan College, Pune

B.L.K. Somayajulu
Physical Research Laboratory, Ahmedabad

Abstract

Humans have inhabited the earth for at least the last 2.5 million years (myr) [Dennell et al., 1988]. They developed art, culture, religion and technology for survival and expansion, and spread over the globe looking for better and perhaps safer areas. This story is reconstructed on the basis of articles left behind during that period. The general region of South Asia that encompasses India has been the home of man for at least the last 700,000 years. Stone tools are the most common record of ancient man in India. Metals and pottery came much later.

While stone tools have been recovered from many parts of India for over a century, it is only in the last few decades that any of the tool occurrences were dated by absolute dating methods (Table 1). These have been invaluable in revising the chronology of the Indian Stone Age and have shown that the ages of the various stages in the evolution of the stone tools have been similar in the Indian subcontinent to that in the rest of the world. In particular, the dating of the volcanic ash associated with the Early Acheulian industry at Bori to 670 kyr, the demonstration that quite a few of the Acheulian sites are older than 350 kyr, the dating of the Middle Palaeolithic to the last interglacial at Didwana, and the large number of dates going back to the limits of radiocarbon dating for the Upper Palaeolithic are of crucial importance.

We present here the geochronological evidence for the presence of ancient hominide in South Asia (India in particular) and discuss the significance.

Geochronology

In simple terms, geochronology is dating, i.e., to find out when the object under consideration came into existence. Dating is the key to placing objects in chronological order [Somayajulu, 1990]. When applied to Archaeology, it relates to dating artifacts that we inherited from our ancestors. Not all artifacts can be dated directly. Wooden items, grains, cloth, plant and animal products and pottery are amenable to direct dating. Stone tools, in principle, are datable but those dates refer to the age of formation of the rock from which the tool was made rather than the time when the rock was transformed into a tool (a hand axe or a cleaver, etc.) (Fig. 1). Therefore, one looks for something

Table 1 Commonly employed dating methods for archaeological samples

Method	Dating Interval (Years)	Principle	Measurement Technique(s)	References
K-Ar	10^5 – 10^9	Decay of naturally occurring ^{40}K (which is 0.012% K) by electron capture or positron emission into ^{40}Ar with a half life of 1.26×10^9 yr.	Mass Spectrometry for ^{40}Ar and Atomic Absorption Spectrophotometry (AAS) for K.	Faure
^{39}Ar – ^{40}Ar	10^5 – 10^9	Same as above except ^{39}K is converted to ^{39}Ar by neutron activation. All measurements are made on the same sample.	Mass Spectrometry for ^{39}Ar and ^{40}Ar after neutron activation of the sample.	Faure; Korisettar et al. (1989)
^{238}U	10^5 – 10^8	Spontaneous fission of ^{238}U with a half life of 1×10^{16} yr in uranium containing transparent minerals.	Etching and counting fission tracks followed by α -particle spectroscopy.	Faure
^{230}Th	10^3 – 10^5	There are two methods using ^{230}Th . Alpha decay of unsupported ^{230}Th (half life = 752,000 yr) is one. The other involves growth of ^{230}Th into radioactive equilibrium with ^{234}U in minerals containing U but no Th.	Radiochemistry and electroplating followed by α spectroscopy.	Krishnaswami & Sarin (1976); Baskaran et al. (1989)
^{14}C	10^2 – 10^4	Beta decay of CR produced ^{14}C with a half life of 5730 yr in carbon containing samples.	Proportional counting of CO_2 , C_2H_2 or CH_4 . Recent technique is AMS.	Agarwal & Kusumgar; Rajagopalan & Vishnu-Mittre (1977); Donahue et al. (1990)

contd.

Table 1 *contd.*

Method	Dating Interval (Years)	Principle	Measurement Technique(s)	References
Thermoluminescence (T.L.)	10^3 – 10^5	Trapping of electrons in dielectric solids in sites of crystal defects due to ionising radiation and subsequent release of the excess energy when heated to about 450° C.	Proper selection of suitable crystals in darkness and measurement of the luminescence as a function of temperature using photomultiplier.	Faure; Singhvi et al. (1982)
Magnetic reversal	10^5 – 10^8	Reversals in the Earth's magnetic field direction at known times in the Pleistocene. Sequential reversals in a well documented stratigraphic column will yield ages for the respective depths of detection of normal-reversed directions.	Collection of oriented samples (preferably) and measurement of intensity and direction of Natural Remnant Magnetisation (NRM).	Faure; Opdyke (1972)

that is associated with the stone tools which can be dated. In these cases, the context between the datable material and the tools would have to be well established. Geological, geomorphological and stratigraphic investigations at the site of excavation and general surroundings assume great importance in order that a meaningful explanation of the 'dates' be obtained. It is equally important that the dated material be as unrecrystallised/unweathered as possible. It may not be out of place to add here that all the dating methods are based on certain assumptions (quite a few of which are common) and the sample has to satisfy/meet these assumptions to have a meaningful date. A number of dating techniques have been applied to archaeological samples; a brief account of these is given in Table 1. It should be mentioned here that two geological terms are in common use for the recent time span (~2 myr) of the earth's history—Pleistocene and Quaternary [Holmes, 1965; Whitten and Brooks, 1976]. Both apply to approximately the same time period. Bifacial axes date back to around a few million years and the earliest stone tools may date before the Quaternary. A list of important dates obtained pertaining to Indian heritage are given in Table 2.

The discussion starts from past (Lower Pleistocene) to present (Holocene). While Indian Palaeoliths (pertaining to the Old Stone Age) are highlighted, the oldest found in other parts of the globe are mentioned and discussed for the sake of continuity.

Table 2 *Ages obtained for Palaeolithic tools and pottery from India*

Site	Material dated and its connection with artifact	Method employed	Age (kyr)	Reference
Bori, Maharashtra	Volcanic ash associated with Lower Palaeolithic tools	K-Ar	537 ± 47	Horn et al. (1993)
		Ar-Ar	670 ± 3	Mishra et al. (1995)
		F-T	640 ± 29	Whitten & Brooks (1976)
Hiran Valley, Saurashtra, Gujarat	Miliolite lying over Lower Palaeolithic tools	U-Th	69 – 190	Baskaran et al. (1986)
—do—	Miliolite lying over Middle Palaeolithic tools	U-Th	> 57	Baskaran et al. (1986)
Nevasa and Yedurwadi, Maharashtra	Carbonate cement overlying Lower Palaeolithic tools	U-Th	> 350	Kale (1990)
Inamgaon, Maharashtra	Fresh water shells associated with tools	¹⁴ C	18.75 ± 0.35	Agarwal & Kusumgar (1975)
Kurnool, AP	Burnt caves	T.L.	17.4 ± 10%	Nambi & Murthy (1981)
Sringa Verapura (Ramayana site) Allahabad, UP	Several pottery samples	T.L.	(2.7 – 3.0) ± 10%	Singhvi et al.

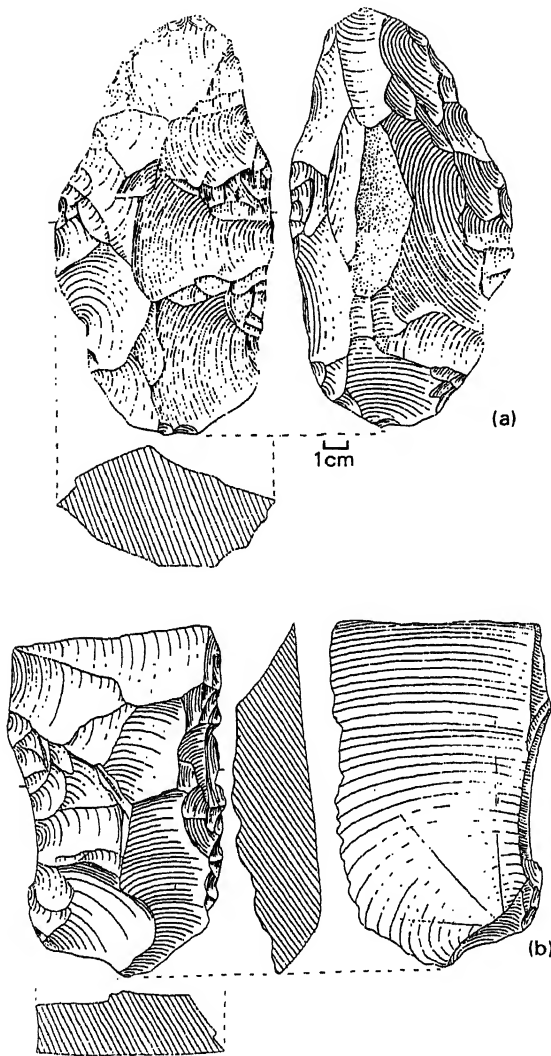


Fig. 1 *Hand-held large cutting tools of the Lower Palaeolithic. (a) Hand axe from Kholar Nadi, District West Nimar, M.P. (b) Cleaver from Mandara, District West Nimar, M.P.*

The earliest tools found in Africa, called Oldoway, do not show any planned pattern of shaping beyond that caused by the mechanics of breaking stone. The next advance in stone tool making is the appearance of deliberately shaped large tools, called handaxes or cleavers (Fig. 1), which is the hallmark of the Acheulian [Mishra, 1992]. The earliest Acheulian has been dated to about 1.5 myr in Africa, and handaxes continue to be found in upto about 40,000 years ago. However, by about 200,000 years before present (BP), there was a change in the technology of flaking stone. This is called the Middle Palaeolithic.

The Middle Palaeolithic period represents a change in stone tool technology from the hand-held bifacial handaxes and cleavers to finger-held flake tools (Fig. 2). The flakes, which were used even earlier in the Lower Palaeolithic, now have definite edge modifications, called retouch, which show their use over a longer duration of time. Resharpenering of the flake edges by repeated retouching has been found in some Middle Palaeolithic assemblages. The Upper Palaeolithic marks a further change in the stone tool technology. For the first time, tools become too small to be held in the fingers or hand (Fig. 3). In the Upper Palaeolithic, composite tools become common. The stone parts of the tools are made of elongated flakes (called blades) which were systematically struck from special cores. These blades were blunted along one side and hafted in handles made from wood, bone or antler.

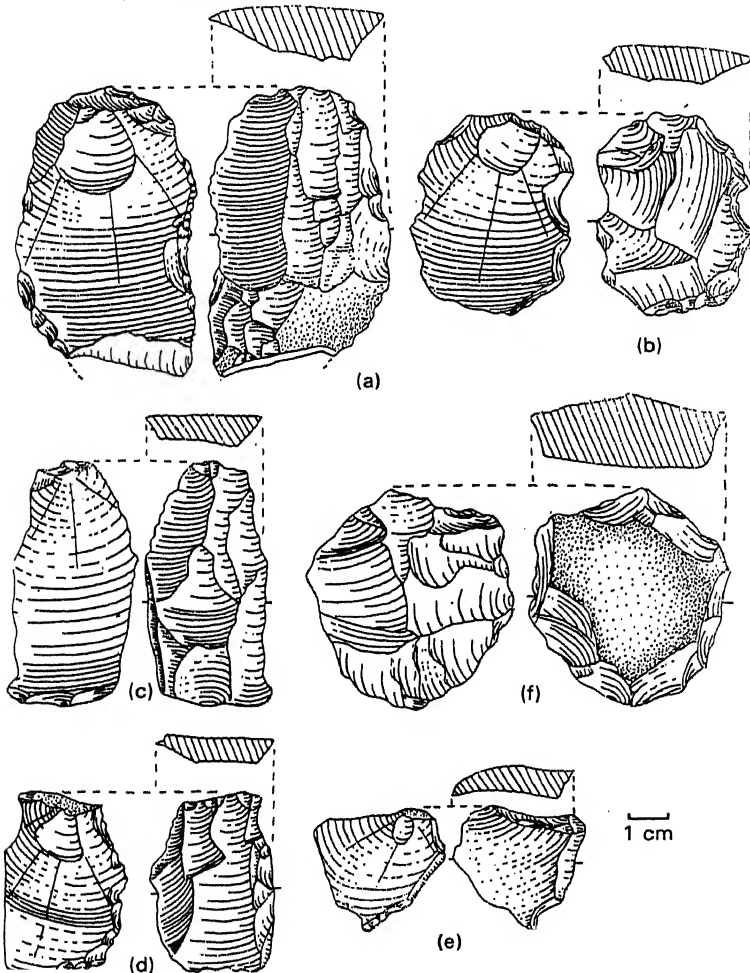


Fig. 2 Finger-held small cutting tools of the Middle Palaeolithic. (a–e) Small flakes with various types of working on the edges. (f) Core showing special preparation to remove flakes.

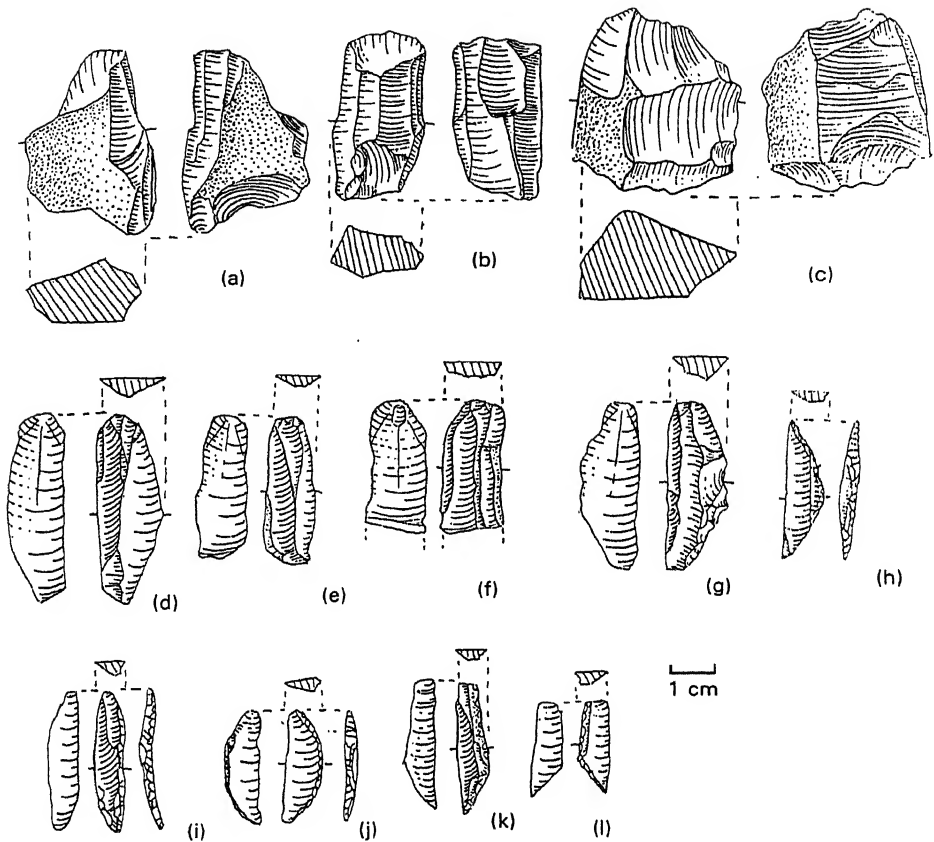


Fig. 3 Blade tools of Upper Paleolithic. These tools are too small to hold in fingers and were halfted into handles. (a–b) Cores for obtaining flakes. (c) Stone nodule showing initial preparation for removing blades. (d–f) Blades. (g–i) Backed blades.

The first evidence of art comes from the Upper Palaeolithic period and most of the industries are associated with fully modern forms of man. The Upper Palaeolithic phase which dates between 40–10 kyr, belongs to the end of the last Ice Age [Dennell et al., 1988].

Lower Pleistocene (2 myr to ~0.7 myr)

Only one site, i.e., Riwat in Pakistan, has been placed in this period. At this site, an artifact was extracted in a gravel bed tilted in the last episode of Himalayan folding. Based on the observation that palaeomagnetic reversal could be identified in sediments overlying the tool and normal sediments containing the tool, the artifact was correlated to Olduvai event which dates to about 2 myr [Dennell et al., 1988; Somayajulu, 1990; Faure].

Middle Pleistocene (0.7 myr to 0.125 myr)

In the sub Himalayan region and peninsular India including Saurashtra, stone tools were discovered and dated.

(i) **Sub Himalayan region:** Stone tools were found in the sub Himalayan zone in the recent Siwalik sediments just above the Brunhes/Matuyama magnetic reversal which is dated to 0.69 myr. An age of 0.4–0.6 myr has been assigned to the handaxes [Mishra, 1992].

(ii) **Peninsular region:** In the peninsular region of India, a number of sites have recently been dated to the early Middle Pleistocene. A variety of dating methods and materials have been used in obtaining ages from this time period. At Bori, the volcanic ash was dated by a number of different techniques, with good agreement between them. Th/U dating of calcretes, miliolite and animal fossils has also contributed to the chronology of the Lower and Middle Palaeolithic period.

Bori: Dating the volcanic ash

The discovery of a volcanic ash layer in association with Acheulian artifacts at Bori was important, in that a rare opportunity to apply absolute dating methods applicable to the Early and Middle Pleistocene was found. At this time, Th/U dating of the ash was done, which showed it to be beyond the range of Th/U dating (>350 kyr). Horn et al. (1993) obtained a sample of the Bori ash and showed that the magnetic minerals in the ash had anomalously high ages. They dated the non-magnetic fraction and got K/Ar age of 538 kyr, Fission Tract age of 640 kyr and T.L. age of 23 kyr. We have [Mishra et al., 1995] obtained an Ar/Ar date for the non-magnetic fraction as 640 kyr (Table 2). The Bori tephra is therefore one of the most thoroughly dated tephtras in the world. The archaeological and geochronological studies at Bori therefore indicate that the age of the Bori tephra is around 600–700 kyr.

Miliolite in Saurashtra

The first dated Acheulian sites in India were Umrethi and Adi Chari Wao, where handaxes were found in gravels capped by miliolite limestone. These dates therefore are the minimum dates for the stone tools. At Adi Chari Wao, the miliolite limestone overlying the stone tools was dated by our above study to 69 kyr and at Umrethi to 190 kyr [Mishra et al., 1995]. The only site that has been dated towards the end of Middle Pleistocene is a tool-bearing site near the 16R Site in Didwana, Rajasthan and data there yield an age of 200 kyr.

Late Pleistocene (125 kyr to present)

During the Late Pleistocene, Upper Palaeolithic stone tool technology was well developed in South Asia. The radiocarbon dating technique is applicable to this time period and so

a large number of sites have now been dated. The sites range in age from 40 kyr to 10 kyr. Several historical sites containing pottery were well dated (Table 2).

The dominant features of South Asian culture and society as seen today developed not during the early Pleistocene, but towards the end of it viz., 10 kyr BP, which is known as the Holocene. The adaptation of plant-animal domestication in the mid-Holocene (4–5 kyr) and then the development of complex societies have left their imprint on present day life. More and more excavations carried out in different parts of the country (and of the globe too) would have to be dated in order to enrich human heritage.

References

1. Agarwal, D.P. and Kusumgar, S. (1975). *Curr. Sci.* **44**, 149–151.
2. Agarwal, D.P. and Kusumgar, S. *Prehistoric chronology and radiocarbon dating in India*. Munshiram Manohar Lal Pub., New Delhi.
3. Baskaran, M., Marathe, A.R., Rajaguru, S.N. and Somayajulu, B.L.K. (1986). *J. Arch. Sci.* **13**, 505.
4. Baskaran, M., Rajagopalan, G. and Somayajulu, B.L.K. (1989). *Chem. Geol. (Isot. Geosci. Section)*. **79**, 65–82.
5. Dennell, R.W., Rendell, H.M. and Hailwood, E. (1988). *Antiquity*. **62**, 98.
6. Dennell, R.W., Rendell H.M. and Hailwood E. (1988). *Curr. Anthropol.* **29**, 495–498.
7. Donahue, J., Jull, A.J.T. and Toolin, L.J. (1990). *Nucl. Instrum. Meth.* **B52**, 224–228.
8. Faure, G. *Principles of Isotope Geology*. 2nd Edn. John Wiley & Sons, New York.
9. Holmes, A. (1965). *Principles of Physical Geology*. 2nd Edn. The Ronald Press Co., New York. 1288.
10. Horn, P., Muller-Sohius, D., Storzer, D. and Zoller, L. (1993). *Zeitschrift der KDeutschen Geol. Gessellschaft*. **144**, 326.
11. Kale, V.S. (1990). *Tropical Geomorph. Newslett.* **10**, 4–5.
12. Korisetar, R., Venkatesan, T.R., Mishra, S., Rajaguru, S.N., Somayajulu, B.L.K., Tandon, S.K., Gogte, V.D., Ganjoo, R.K. and Kale, V.S. (1989). *Curr. Sci.* **58**, 564–567.
13. Krishnaswami, S. and Sarin, M.M. (1976). *Anal. Chem. Acta.* **83**, 143–156.
14. Mishra, S. (1992). *Curr. Anthropol.* **36**, 847–851.
15. Mishra, S., Rajaguru, S.N. and Somayajulu, B.L.K. (1995). *Curr. Anthropol.* **36**, 847.
16. Nambi, K.S.V. and Murthy, M.L.K. (1981). *Curr. Sci.* **50**, 945.
17. Opdyke, N.D. (1972). *Rev. Geophys. Space Phys.* **10**, 213–249.
18. Rajagopalan, G. and Vishnu-Mittre (1977). *Proc. International Conf. on Low Radioactivity, measurements and applications*, Comenius Univ. 335–340.
19. Rendell, H.M. and Rendell, R.W. (1985). *Curr. Anthropol.* **26**, 293–300.
20. Singhvi, A.K., Agrawal, B.P. and Nambi, K.S.V. In *Recent advances in Marine Archaeology*. Proc. Second Indian Conf. on Marine Archaeology of Indian Ocean Countries. S.R. Rao, ed. National Institute of Oceanography, Goa. 173–180.
21. Singhvi, A.K., Sharma, Y.P. and Agarwal, D.P. (1982). *Nature*. **259**, 313–315.
22. Somayajulu, B.L.K. (1990). *Man & Environ.* **11**, 1–11.
23. Whitten, D.G.A. and Brooks, J.R.V. (1976). *A Dictionary of Geology*. Penguin Books, U.K. 495.

8

Rapid climatic shifts and its influence on ancient civilisations: Evidence from marine records

Pothuri Divakar Naidu

National Institute of Oceanography, Dona Paula, Goa

Abstract

The southwest (SW) monsoon system in the Arabian Sea exerts a strong influence upon the climatic conditions in South and Southeast Asia, and the associated monsoon rainfall has a great impact on the socio-economic and agricultural development in the densely populated South Asian region. Studies on the variability of the SW monsoon for the last 19,000 years before present (BP) by using marine sediment records reveal that the SW monsoon started its intensification from 12,000 years BP after a weak phase during the last glacial period. During the Holocene period, the weakening of the SW monsoon started from 5,000 years BP and the intensity of monsoon returned to glacial strength at 3,500 years BP, coinciding with the onset of arid climate elsewhere in the tropics. The onset of weak phase of the monsoon and arid climate at 3,500 years BP appears to be a primary reason for the decline of the Indus Valley Civilisation, major changes in vegetation along the Western Ghats and decrease of river discharge from all major rivers during that period. Similarly, the Classic Maya Civilisation of Central America collapsed around AD 750–900 due to rapid climatic change during that period in Central America. These evidences suggest that climatic changes have a bearing on ancient civilisations and human heritage.

Introduction

The word ‘monsoon’ is derived from the Arabic word ‘mausim’ which means season. Winds blow from the ocean to land during the summer and from land to ocean during winter in the Indian Ocean. This seasonal reversal of the wind direction between summer and winter drives the southwest and northeast monsoons in the Indian Ocean and causes precipitation in South Asia. The fundamental mechanism of the monsoon is (i) the differential heating of land and ocean and the resulting pressure gradient that drives the winds from high pressure zones to low pressure zones, (ii) the swirl introduced to the winds by the rotation of the earth, and (iii) moist processes that determine the strength, vigour and location of the major monsoon precipitation.

In the northern hemisphere, during summer, high solar radiation causes intense direct and latent heating over Central Asia, especially over northern India and the Tibet Plateau.

The pattern of heating causes an ascending air flow to the atmosphere, which leads to the development of an intense low pressure cell that is centred over Asia. At the same time, a high pressure cell develops over the southern Indian Ocean due to the southern hemisphere winter and the greater specific heat of water. Thus, an atmospheric pressure gradient between the Asian continent and the cooler southern Indian Ocean induces a large-scale meridional overturning, with the lower circulation limb being the strong low level SW summer monsoon winds of the western Indian Ocean (Fig. 1). These marine air masses converge over the Indian subcontinent and are uplifted due to heating and orographic steering, which causes seasonal monsoon rains in South Asia.

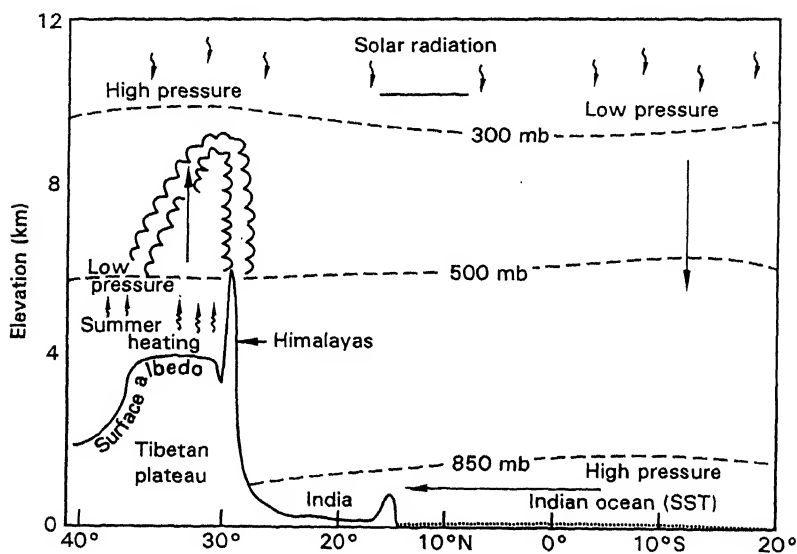


Fig. 1 *The conceptual model of boundary conditions and climate process which manifests onset of monsoon in the Indian Ocean*

Link between monsoon, upwelling and sediment record

The SW monsoon winds drive the intense upwelling off Oman and Somalia and sporadic upwelling along the southwestern coast of India. The strength of the SW monsoon winds, upwelling in the Arabian Sea, and precipitation in South Asia are strongly coupled. These upwelling waters are characterised by cooler temperature and enriched phytoplankton biomass. Distinctive planktonic flora and fauna thrive in these upwelling waters. Northeasterly winds during winter suppress upwelling and lower the productivity in the western Arabian Sea. Thus, the southwesterly and northeasterly winds produce a striking seasonal contrast in primary productivity in the Arabian Sea. Sediment trap mooring experiments demonstrate that the biogenic and lithogenic flux supply to the sea bottom is strongly correlated with monsoon winds. Thus these seasonally dominant

particles eventually settle onto the seabed to form a distinct biogeochemical record of upwelling. The upwelling and associated productivity events are largely driven by what is technically termed as Ekman transport; their duration and intensity reflect the structure and strength of the monsoon winds.

Most of the developing countries are situated within the tropical and monsoon influenced regions of the world. Agricultural production in these countries is critically influenced by weather, and these countries are predominantly dependent upon agriculture; their overall performance is highly sensitive to weather uncertainties. In the absence of monsoons that bring adequate rain, life styles can be seriously and, occasionally, irreversibly disrupted. The first effect of insufficient rains is crop yield reduction or crop death. In addition, recurrent drought may cause a serious shortage of drinking water for humans and animals. Water reservoir levels drop, reducing the generation of hydroelectric power, and the resulting energy shortages limit agricultural and industrial production. The unique monsoon circulation in the Indian Ocean and associated rainfall over South Asia thus have a fundamental impact on the socio-economic and agricultural development in the densely populated Asian countries.

Methodology

Oceanographers go on research vessels and collect sediment cores to reconstruct palaeo-oceanographic and palaeoclimatic history during the geological past. In order to reconstruct

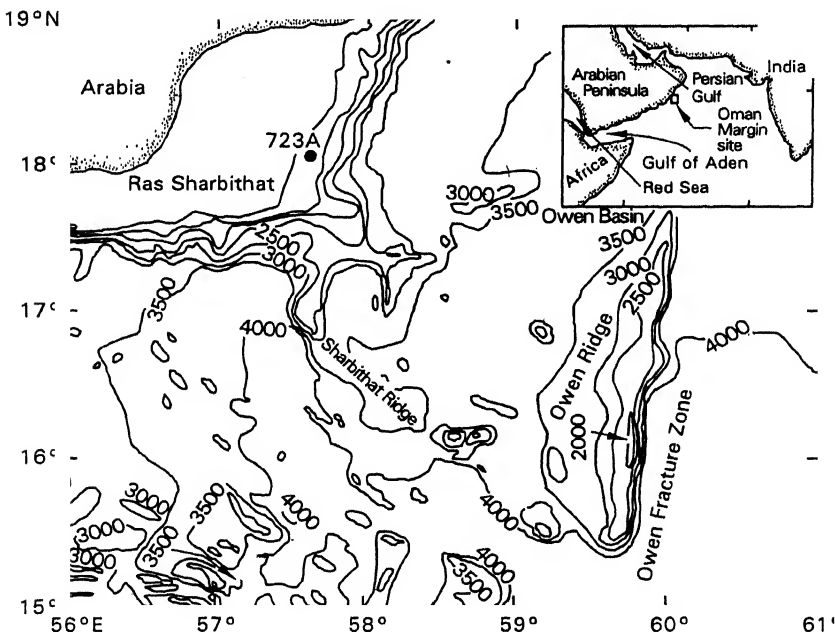


Fig. 2 Location of Ocean Drilling Program Site 723 A and bathymetry

the monsoon variability for the last 19,000 years BP, Ocean Drilling Program (ODP) Site 723A (Fig. 2) was chosen for two reasons: (i) its vicinity to the intense upwelling zone, and (ii) high sedimentation rate, which enables one to carry out high resolution studies. The chronology was established by using Accelerated Mass Spectrometer Carbon-14 dates. The abundance of the planktonic foraminifer species *Globigerina bulloides* in the sediment has been used to monitor the quaternary upwelling history in the Arabian Sea [Prell, 1984; Anderson and Prell, 1993]. The sediment trap experiment in the Arabian Sea also confirms that the flux variation of *G. bulloides* is directly proportional to the monsoon intensity in South Asia [Curry et al., 1992]. Therefore, in the present study, accumulation rates of *G. bulloides* (number of specimens/gram sediment/1000 years), and total planktonic foraminifera were used as proxies of upwelling strength in the Arabian Sea and associated SW monsoon rainfall in South Asia.

Onset of arid climate and its possible effect on the Indus Valley Civilisation

Intensification of the SW monsoon started 12,000 years BP after a weak phase during the last glacial period (Fig. 3). Within the Holocene, greater values of upwelling indices have been noted between 10,000 and 6000 years BP, reflecting a strong SW monsoon. The values of upwelling indices decrease abruptly at 5000 years BP, indicating a weakening phase of the SW monsoon. The lowest upwelling indices in the Holocene occur between 3500 and 1200 years BP (Fig. 3), suggesting that upwelling and the SW monsoon intensity decreased during this period. At 3500 years BP, the upwelling indices exhibit the same values as those at 12,000 years BP, when the monsoon started its intensification after the last glacial period, and from 3500 years BP the upwelling indices decline further. Other evidences such as water levels in Ethiopian lakes [Gillespie et al., 1983], palaeohydrological data from western Tibet [Gasse and van Campo, 1994], benthic foraminifera records from eastern Arabian Sea, pollen records from Northwest India and $\delta^{13}\text{C}$ values of peat deposits also suggest a weaker SW monsoon during this time. A similar pattern of dry conditions during the late Holocene is also reported from Africa and the regions around the Caribbean.

Independent evidences such as pollen studies from the eastern Arabian Sea [Caratini et al., 1994] and downcore variations of calcium carbonate in the western Arabian Sea and $\delta^{18}\text{O}$ data from Tibetan lakes also document the arid climate during this time [Gasse and van Campo, 1994]. This observation is further corroborated by an abrupt change in solar radiation, precipitation, temperature and southeasterly winds at about 3500 years BP in the Arabian Sea [Zahn, 1994]. The declining strength of the SW monsoon since 3500 years BP can therefore be interpreted as a result of the onset of arid climate, in general throughout the tropics, and in particular, in the Asian tropics. The onset of arid climate and decline of the SW monsoon at 3500 years BP resulted in a change in the vegetation along the Western Ghats [Caratini et al., 1994].

The Indus Valley Civilisation was at the height of its glory during the period when Egyptian, Babylonian and Mesopotamian civilisations were existing in present-day Middle East. Archaeologists believe that the Indus Valley Civilisation belonged to the

period between 3500 BC and 2800 BC. Agriculture was the main occupation of the Indus Valley people; crops such as wheat, barley, peas and bananas were grown. It is well established that the downfall of Chalcolithic culture (about 1,000,000 BC) is ascribed to severe droughts in western and central India. Similarly, the decline of the Indus Valley Civilisation from 3500 years BP could be due to the onset of arid climate.

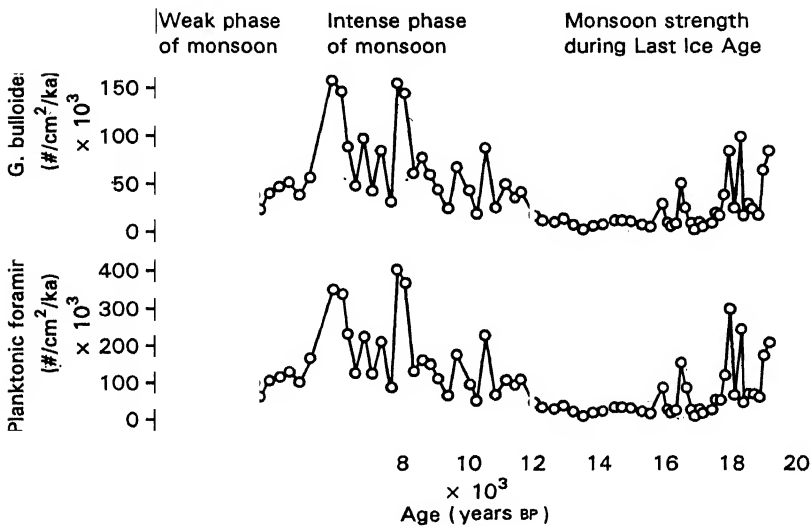


Fig. 3 Variations in mass accumulation rates of planktonic foraminifera and *G. bulloides* through the last 19,000 years BP in Ocean Drilling Program Site 723A from the western Arabian Sea. These microfossil indices are sensitive to upwelling intensity and may, therefore, be employed to monitor the history of the SW monsoon climate in the Arabian Sea and rainfall in Southeast Asia.

Previously, it was reported that about 1500–4000 years BP, the Harappan Civilisation was destroyed due to a great flooding [Nigam and Khare, 1989]. However, the intensity of the monsoon precipitation is at its minimum during 1500–4000 years BP compared to the mid-Holocene precipitation as evidenced from the upwelling record [Naidu, 1995, 1996]. Therefore, the great flooding about 1500–4000 years BP might be a result of rapid weather change for a brief period but not due to intense SW monsoon precipitation.

The Maya Civilisation developed around 3000 years BP in Mesoamerica, and after flourishing during the so-called 'Classic' period, collapsed around AD 750–900. The Oxygen isotope signal in carbonate shell and the gypsum/calcite ratio in the sediments represent past changes of the evaporation to precipitation ratio—here the working assumption is that the times of high evaporation to precipitation ratio (dry climate) are reflected by increased $\delta^{18}\text{O}$ values of shell carbonate and an increased proportion of gypsum to calcite in sediments. Conversely, periods of low evaporation to precipitation ratio (wet climate) are marked by low $\delta^{18}\text{O}$ values and a decreased proportion of gypsum to calcite. The onset of driest climate between AD 800–1000 (Fig. 4) was reported in

Central America based on variation of $\delta^{18}\text{O}$ and gypsum to calcite ratio in a sediment core from Lake Chichancanab [Hodell et al., 1995]. The timing of this climate drying corresponds approximately to the collapse of the classic Maya Civilisation between AD 750–900. Although it is difficult to decipher the cause-and-effect relationship, the observed association between the drier climate at 3500 years BP and between AD 800 to 1000 and their coincidence with the collapse of the Indus Valley Civilisation and Maya Civilisation respectively, makes a point that climate has played a role in the extermination of ancient civilisations. These evidences should be intriguing to anthropologists studying the evolution and adaptation of ancient civilisations.

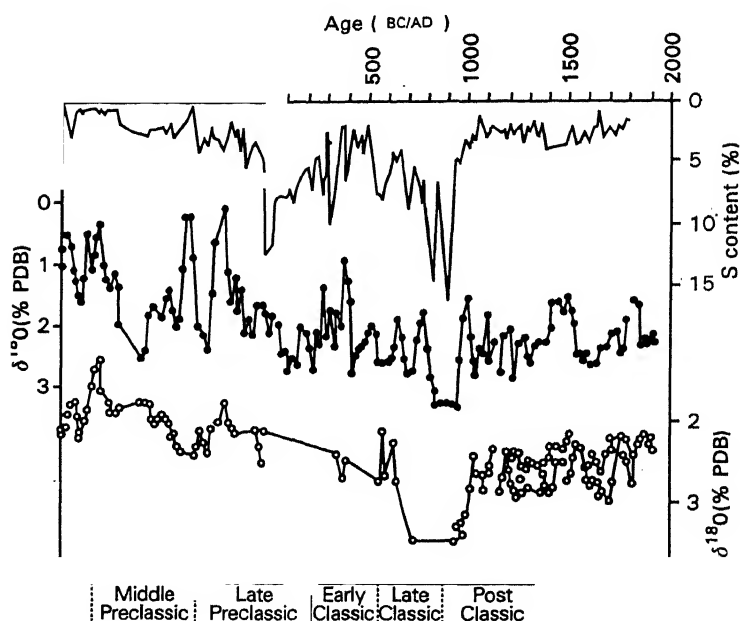


Fig. 4 Sulphur content and $\delta^{18}\text{O}$ values plotted versus calendar years. Proxy signals of palaeoclimate are compared with major subdivisions of Maya cultural evolution. The peaks in total sulphur content and $\delta^{18}\text{O}$ values are centred at AD 900 and indicate increased aridity during the terminal 'Classic' Period

Impact of rapid climatic shifts on human intelligence

The essence of intelligence is cleverness, a versatility in solving novel problems. Human intelligence was not developed in a single stroke but evolved gradually through millions of years. Calvin (1994) argues that human intelligence arose primarily through the refinement of some brain specification, such as that for language. The specialisation would allow a quantum leap in cleverness and foresight during the evolution of humans from apes. The four-fold expansion of the hominid brain occurred only after the Ice

Ages began 2.5 myr ago. The Oxygen isotope records of Greenland ice core (Fig. 5) and marine sediment cores from oceans from any part of the world clearly show frequent abrupt cooling periods superimposed on the more rhythmic ice advance and retreat. Entire forests and other vegetation disappeared all over the globe for several decades because of drastic drops in temperature and rainfall. The temperature rose and rainfall increased with equal suddenness several centuries later. Such cold and warm periods occurred cyclically for the last 2.5 myr. In the present context, discussion is focussed on the changes that occurred during the Last Ice Age (cold period) and the Current Interglacial Period (warm period). The Oxygen isotope record of Greenland ice core clearly displays the climatic fluctuations for the last 250,000 years (Fig. 5). The climate flip which occurred at the transition from the Last Glacial Period to the Current Interglacial Period resulted in a 13°F (7.2°C) temperature rise, a 50% increase in rainfall, and a reduction in the severity of dust storms, all in the space of a few decades. Cold periods began just as suddenly. The evolution of anatomical adaptations in the hominids could not have kept pace with these abrupt climate changes, which would have occurred with the life time of humans. Still, these environmental fluctuations could have promoted the incremental accumulation of mental abilities that conferred greater behavioural flexibility.

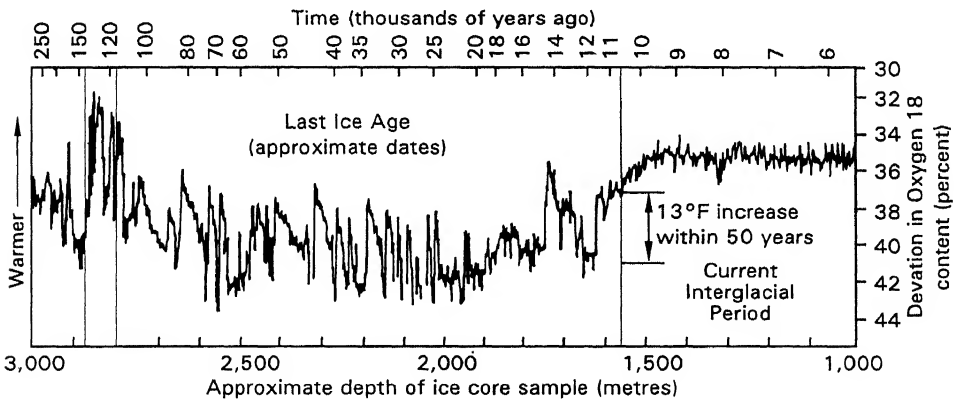


Fig. 5 Oxygen isotope variations of Greenland ice core during the Last Ice Age and the Current Interglacial Period. The arrows indicate a rise of temperature by 13°F within 50 years.

The Greenhouse effect and society

The *greenhouse effect* is a geographical fact of life. For the last ten years the problem of greenhouse gases and its impact on the future climate has drawn considerable attention from palaeoceanographers and atmosphere chemists. Atmospheric gases such as carbon dioxide and methane store heat, enabling the Earth's biota to survive. Such gases have warmed the surface of this planet by about 33°C, from below freezing to a current average of about 17°C. Models and analyses of global warming generally agree that

most of the long-lived gases that human activity adds to the atmosphere make the Earth warmer than it would otherwise be. The recently held historic summit on global climate, in Rio de Janeiro, also emphasised the real need to control the emission of greenhouse gases to protect the planet. Predicted warming based on recent increases in concentration of greenhouse gases is slightly more than the observed warming trend of the atmosphere. In addition, the warming trend in North America does not appear to follow the global pattern. Very recently, Gupta et al. (1996) reported that the greenhouse gases may not increase the sea surface temperature the way it was believed to; on the other hand, sea surface temperature fluctuates and the intensity of the greenhouse effect is modulated by the Milankovitch cycles of the Earth's orbit. If the increasing concentration of greenhouse gases causes any rapid warming, whether it has positive or negative effects on society is yet to be dealt with in detail.

Recently, Keigwin (1996) documented the Little Ice Age and medieval warm events in the sediment records of Sargasso Sea and concluded that the persistence of warming trend is at its natural warming limb. It is important to distinguish between natural climate change and anthropogenic effects because human influence may be occurring at a time when the climate system is on the warming limb of a natural cycle.

Summary

The SW monsoon system in the Indian Ocean exerts a strong influence upon the climatic conditions in South and Southeast Asia. The strength of the SW monsoon winds, upwelling and rainfall in Southeast Asia are strongly coupled. Thus the reconstruction of upwelling intensity in the Arabian Sea reveals the quantity of rainfall caused by the SW monsoon winds. The intensity of the SW monsoon was at its peak during the mid-Holocene period and it reached glacial level at 3500 years BP which coincides with the onset of arid climate globally. The onset of arid climate at 3500 years BP might be one of the primary reasons for the fall of the Indus Valley Civilisation. Similarly, the Maya Civilisation collapsed in Central America during AD 1000–700 due to the influence of unforeseen warm climate.

The above evidences support the concept of climate change and its impact on ancient civilisations. Humans, fauna and flora can withstand gradual climate changes but drastic, sudden and rapid changes might have a negative effect on the survival of all life forms. On the other hand, these may pose a challenge to adapt to the changes.

References

1. Anderson, D.M. and Prell, W.L. (1993). A 300 kyr record of upwelling off Oman during the Late Quaternary: Evidence of the Asian southwest monsoon. *Paleoceanography*, **8**, 193–208.
2. Caratini, C., Bentaleb, I., Fontugne, M., Morzadec-Kerfourn, M.T., Pascal, J.P. and Tissot, C. (1994). A less humid climate since ca. 3500 yr BP from marine cores off Karwar, western India. *Paleogeography Paleoclimatology Paleoecology*, **109**, 371–384.
3. Calvin, W.H. (1994). The emergence of intelligence. *Sci. Am.* October 1994. 79–85.

4. Curry, W.B., Osterman, D.R., Guptha, M.V.S. and Ittekkot, V. (1992). Foraminiferal production and monsoonal upwelling in the Arabian Sea: Evidence from sediment traps. In: C.P. Summerhays, W.L. Prell and K.C. Emeis (eds.), *Upwelling System: Evolution Since the Early Miocene*. Geological Society, London. 93–106.
5. Gasse, F. and van Campo, E. (1994). Abrupt post glacial climate events in West Asia and North African monsoon domains. *Earth and Planetary Science Letters*. **126**, 435–456.
6. Gillespie, R., Street-Perrott, F.A. and Switzur, R. (1983). Post glacial arid episodes in Ethiopia: Implications for climate prediction. *Nature*. **306**, 680–683.
7. Gupta, S.M., Fernandes, A.A. and Mohan, R. (1996). Tropical sea surface temperatures and the Earth's orbital eccentricity cycles. *Geophy. Res. Letts*. **22**, 3159–3162.
8. Hodell, D.A., Curtis, J.H. and Brenner, M. (1995). Possible role of climate in the collapse of Classic Maya Civilisation. *Nature*. 375–394.
9. Keigwin, L.D. (1996). The Little Ice Age and Medieval Warm Period in the Sargasso Sea. *Science*. **274**, 1504–1508.
10. Naidu, P.D. (1995). High-resolution studies of Asian Quaternary monsoon climate and carbonate records from the equatorial Indian Ocean. *Ph.D. Thesis*. Gothenburg University, Gothenburg. 36.
11. Naidu, P.D. (1996). Onset of an arid climate at 3.5 ka in tropics: Evidence from monsoon upwelling record. *Curr. Sci*. **71**, 715–718.
12. Nigam, R. and Khare, N. (1992). Oceanographic evidences of the great floods in 2000 and 1500 BC documented in archaeological records. *Proceedings of New Trends in Indian Art and Archaeology*. 517–522.
13. Prell, W.L. (1984). Variation of monsoonal upwelling: A response to changing solar radiation. In A.L. Berger, J. Imbrie, J. Hays, G. Kukla and B. Saltzman (eds), *Milankovitch and Climate*. D. Reidel, Hingham. Part 1, 349–366.
14. Zahn, R. (1994). Fast flickers in the tropics. *Nature*. **372**, 621–622.

9

The people of India: Diversities and linkages

K.S. Singh

Saket, New Delhi

Over the last twelve years the Anthropological Survey of India (ASI) has been engaged in generating, retrieving, compiling and analysing a vast amount of data on the human heritage of India. In 1984, fresh initiative was taken to retrieve, compile and analyse the data on the anthropometric survey of India undertaken in the 1960s [Basu and Sreenath, 1995, 1996; Sreenath and Ahmed, 1989; Sreenath and Basu, 1996] and the dataset yielded by the All India Bio-anthropological Survey initiated in the 1970s [Ghosh, 1988]. The two datasheets have already been published in many volumes and the remaining volumes are likely to be published in a couple of years. Similarly, the data on the survey on linguistic traits, undertaken in the 1970s, has been published [Shree Krishan, 1990].

In this background the ASI launched the People of India Project (POI) on October 2, 1985 with a view to generating a brief descriptive anthropological profile of all communities of India, the impact on them of change and development and the linkages between them. The format, both structured and open ended, had four parts. The first related to the ethno-origin and distribution of communities and their self-perception, the second dealt with social organisation of the community, the third with economy and the impact of change and development, and the fourth and last one explored the linkages, both traditional and modern, among communities. Ethnography has a continuing tradition. However, in colonial times, ethnographic communities were primarily studied as islands. The post-colonial ethnography explores the linkages and relationships of the communities engaged in the task of nation building on multi-ethnic and multi-cultural societies. The honeycomb model of interaction was suggested for such societies in which communities are engaged in the process of vibrant interaction.

The logistics

Over almost a decade following the launching of the project, it has been possible to identify, locate and study 4694 communities in all States/Union Territories of India and computerise the data for this large number of communities. Yet in spite of all efforts to identify all communities there still remains a grey area, though a small one, where identities are still fluid, and identification is problematic. The communities thus identified included the scheduled tribes (461), scheduled castes (445) and other communities. The transfer of the data to computers started at an early stage in March 1988, and for

the first time in the country a software was developed in ethnography, which was also probably among the first of its kind in the world. This was a vast participatory project in which not only scholars from all parts of India and at all levels had participated, but also the people and local scholars who not only generated information but also wrote out the material. Therefore at one stage this project was described as a project on the people of India by the people of India. 470 scholars participated in this project including 245 from outside the ASI. Twentysix institutions other than ASI were involved in it. About 120 workshops and rounds of discussions were held in all States/Union Territories in which about 2000 scholars participated to plan the studies and evaluate the findings. The investigators spent 24,880 days in the field and interviewed 21,536 people, of whom 5,353 were women, in villages (4,513), mostly multi-community villages, and in towns (941) spread over most of the districts (438) and eco-culture regions as identified under the project. The states were thus further divided into about 96 natural eco-cultural zones defined by dialects, folklore, history, administration and so on. About 21,362 photographs covering 2548 communities were generated to build up the visual documentation of the people of India. A large number of maps showing the distribution of the communities were also prepared.

The project was entirely *swadeshi*, or homespun. All knowledge is both universal and specific, and anthropology as a branch of knowledge is closely related to culture and environment. In this discipline every culture is unique, and every trait is unique. This project also sought to explore the idioms, the structures and the cognitive processes reflected in the understanding and perception of people about themselves, and their relationship with one another and with the environment.

The above surveys covering biological, linguistic and cultural dimensions which have evolved in tandem, seek to generate a composite profile of all the people of India. Each community is covered in terms of biological variation, linguistic traits, and cultural and socio-cultural aspects. The output is enormous. Out of the 43 volume POI project, 23 volumes have already been published and the remaining volumes are to be published over the next two to three years. Thus by the end of the century we should have a large corpus of materials running into about 100 volumes covering the biological, linguistic and cultural profiles of the people of India.

It is interesting to note that the explosion of so much information—and so much knowledge—about people has coincided with similar developments at the international level. In fact, in no other period of human history has so much information and so much knowledge been generated and disseminated about people and about diversities. With this knowledge of diversities, a new notion of community—or the old notion reinforced by current concerns—has emerged. This is the notion of a community rooted in its environment, its resources, and in various networks of relationships. The environmental movements, the movement of the indigenous people, the ethnic explosion, and many other developments have tended to converge and reinforce the notion of a community, irrespective of labels, as something far more basic in its formation than we have understood so far.

Yet another development has been an attempt to establish linkages where they exist among diversities of all kinds. There is a wide range of information today on biodiversity which is now being linked up with linguistic and cultural diversities. In fact, all three dimensions are closely related, each reinforcing the others.

The people of India derive their identity from India, i.e. *Bharat*. The notion of *Bharat* which has evolved, came to be applied to the landmass lying south of the Himalayas, bounded by the oceans. The authors of the *Puranas* have written about this territorial configuration. Poets from Kalidas to Rabindranath Tagore and Subramania Bharati have eulogised it. It was in the course of the freedom struggle that this territorial identity was fused with deep emotion, as compositions glorifying the land and seeking freedom for it—it was described as *Mata, Bharat Mata*—poured out in various languages: Jawaharlal Nehru said that *Bharat Mata* was the people of India.

Biological diversity of the people

DNA-based studies should tell us finally about the pattern of the peopling of the subcontinent. All that is known for definite at this stage is that the *Homo sapiens sapiens* originated in eastern Africa from where they migrated in waves upon waves to different parts of the world including our own. According to the present estimates, Australia was peopled about 40,000 bc and the Americas around 15,000 bc. Rough estimates for the peopling of India given by scholars belonging to various disciplines are 60,000 bc for the Australoid and 15,000 bc for the Caucasoid. Even without going so much into prehistory, it could be mentioned that different communities of India recall their recent or not-so-recent migration in their oral traditions, *jati puran* and history. Migrations have varied in range. An Indian is a migrant par excellence. Communities have settled in different ecological and climatic regions of India and derive their identity from hills and valleys, the plains, islands and villages—particularly the ancestral villages.

The communities are rather unevenly distributed in all States and Union Territories. By far the largest number of communities (above 350) are in Andhra Pradesh and Tamil Nadu. They vary between 250 and 350 in Uttar Pradesh, Bihar, Madhya Pradesh, Maharashtra, Orissa, Karnataka and Gujarat. The range varies from 150 to 250 communities in West Bengal, Rajasthan and Kerala. Arunachal Pradesh, Assam, Tripura, Jammu and Kashmir, Himachal Pradesh, Haryana and Punjab have communities ranging from 50 to 150. The number of communities drops to below 50 in Nagaland, Manipur, Mizoram, Meghalaya, Sikkim, Goa, Chandigarh, and the Bay islands. Each State/Union Territory has been treated as a unit of our study. The various stated regions of India are not only politico-administrative units; they are also linguistic units and they are also ethnic units because most communities (72%) are located within each one of them. Only a few of them (about 24%) are distributed over adjoining areas, and about 4% of them are distributed over a larger part of the country.

Probably nowhere in the world have there existed so many communities—4694 including the main communities (2205), major segments (589) and territorial units (1900). These communities have been identifying themselves in various ways through history, by territory, by *varna* and *jati*, by occupation and so on. In addition to the names or nomenclatures of communities there is an impressive range of synonyms, surnames and titles. No community is without divisions and there are a large number of segments.

Linguistic diversity

The diversities in terms of linguistic traits are wide ranging. There are as many as 325 languages divided into five language families. Twentyfive scripts are in use. The linguistic situation is heterogeneous at one level because the Indians have a natural ease with language and most of them speak a number of languages, or at least two languages. And yet it is fascinating that many linguistic traits have penetrated across the five language families. India has been variously described as a socio-linguistic area, a single semantic area, a single linguistic and cultural unit. In the language contact situations, the incidence of bilingualism is rather much too conservative (13% estimated in 1981). One of the reasons for this could be mother tongue loyalty. Tribals are trilingual. No state in India is unilingual in spite of the preponderance of the speakers of the scheduled or state language.

Most Indians have been a highly mixed people from the early periods of prehistory or history. The skeletal remains at the rock shelter site in Mirzapur dating back to 15,000 BC and those belonging to the Mohenjodaro-Harappa sites suggest the existence of mixed populations. Though racial classification of populations has now been discarded, morphological and genetic variations among populations are being explored—which, it is stated, are present on a larger scale within a community than between communities. There is thus a greater biological diversity among the people of India than among people elsewhere. Yet their likenesses appear to be more than their differences, and the number of genes in which they differ are only a few in comparison with the vast number of common genes. This may be due to the fact that there were waves of migration on a scale larger than probably anywhere else in the world, and that the mating pattern remained relatively flexible for a long period, making for a free flow of genes. Caste endogamy emerged in its rigid form at a later period in history. Within a region there was a greater admixture of populations and clustering of traits. There is therefore a much greater homogenisation in terms of morphological and genetic traits among communities at the regional level, and most of the communities within a region or state therefore share many traits. This has been brought out significantly in the anthropometric survey of the populations in various states.

Indians have their own notion of beauty as represented by colour and texture of the skin, which is influenced by the climate. There is a whole range of shades from fair to dark complexion, described in various evocative terms in classical literature and folklore, existing together. There is a popular saying that a bride should be fair like Sita and a bridegroom should be pleasantly dark like Rama.

Indians are reported to have relatively large eyes. This may be because our eyes keep popping all the time; there is so much beauty, so much diversity to behold!

As mentioned above, the communities should be best seen in the context of the eco-system and eco-cultural zones, as most of them are rooted in their resources. They derive their identity from their environment, and their occupations are based on their resources. Even the migrant groups seek to assimilate into their new environment except in the matter of the language they speak at home, or in terms of marriage. The rootedness in local eco-cultural system is an outstanding characteristic of our communities, no matter what religious label is attached to them, as Hindus, Muslims, Christians, and so on.

Again, an important feature of our ethnographic scenario has been the range of migration of communities, families and individuals—most of the communities are migrants—across the length and breadth of the country, and their adaptation to local traditions and their contribution to the development of local traditions, even as or before the ‘son of soil’ phenomenon emerged.

Cultural diversity

There is also an extraordinary range of diversities in terms of cultural traits which tend to cluster at various local and regional levels: People cutting across castes and communities share a great deal within an eco-cultural–linguistic region or its sub-region. As many as 775 traits have been identified, relating to ecology, settlement, identity, food habits, social organisations, economy and occupation, linkages, and impact of change and development. Within a region, communities cutting across religions share a great many traits. The sharing of traits has to be seen at some other levels also. For example, it appears that a number of states belonging to a linguistic/cultural region share a very high percentage of traits, for example, Lakshadweep and Kerala, and all other southern states on one hand and the eastern states and non-eastern states on the other hand. Another dimension is the sharing of traits across communities. For instance, if one takes the communities grouped into religious categories, one finds that the Hindus share a very high percentage of traits with Muslims (97.7%), Buddhists (91.9%), Sikhs (88.99%), Jains (77.46%). Other communities which share a high percentage of traits are: Muslim–Sikh (89.95%), Muslim–Buddhist (91.18%), and Jain–Buddhist (81.34%).

Therefore, the traits we share are far more than the traits that we do not share. A reason for sharing of traits on such a large scale could be the fact that most of the communities have emerged from the same ecological, ethnic, socio-cultural background, even though they have later embraced different religions or other ways of life.

Food and drink

In spite of the higher value attached to vegetarianism, only about 20% of Indian communities are vegetarian. There is vegetarianism of all shades and nuances shaped by the compulsions of ecology, value system, availability of food and so on. There are vegetarians who take eggs, fertilised or non-fertilised; there are also vegetarians who abstain from onion and avoid garlic. The men are mostly non-vegetarian. A shift from vegetarianism to non-vegetarianism is reported in many communities, and similarly a shift from non-vegetarianism to vegetarianism is also reported rather weakly, mostly amongst the scheduled castes and tribes (SCs and STs).

With growing affluence, there has also been a sharp increase in the consumption of alcoholic beverages by men. Traditionally women occasionally consume alcohol in a number of communities. Smoking is very common. Chewing of tobacco and the use of snuff are also widespread. Chewing betel is common in a large number of communities. We are, therefore, largely a drinking, smoking and meat-eating people.

Occupations

As many as 42 major occupations and 307 current occupations, bringing the total to 349, have been identified all over the country. With the diversification of the economy and social mobility, a number of occupations are practised by members within a single *jati* or community. There are few communities whose members follow only one occupation. The average number of occupations per community stands at 5.3, of which 1.8 is traditional and 3.5 is the newly acquired occupation. There has been a decline in traditional occupations like hunting, gathering, trapping birds and animals, pastoralism, shifting cultivation, salt-making, and toddy tapping, with shrinkage of resource base, depletion of forests and so on. Settled cultivation is the leading occupation, pursued by members of many communities, followed by wage labour and animal husbandry, fishing, and textile weaving. Of modern occupations, government service is the most sought after; members of as many as 3051 communities reportedly work for the government. Participation is on the increase in business, trade, industrial work, private service and self-employment sectors.

Distinct identities

The regions of India have evolved since the prehistoric period into language areas (since the medieval period) and into politico-administrative units as States (25) and Union Territories (7) today. They have been culturally distinct, the various communities within their ambit sharing a great deal by way of language/dialects, folklore, elements of material culture, customs (*lokachars* and *desachars*), local/regional dress and ornaments, cuisine, and so on. So strong has been the alchemy of regional identities that those who have gone in have become a part of it. If the matrimonial columns of national dailies are an indication, most people want to marry within their language group.

The Constitution of India which speaks of the people of India in a collective sense identifies five groups—the scheduled castes, the scheduled tribes, the religious and linguistic minorities, the educationally and socially backward classes, and the Anglo-Indians. All these groups are spread all over the country. Most of them are rooted in their milieu. They have been heterogeneous in terms of their perceptions of themselves, their differing versions of origin, their kinship structures, their life cycle ceremonies, their occupations which have now diversified, and so on.

The knowledge thus generated of such formations is two-fold. At one level, a community is projected as homogeneous, marked by the birth and sharing of many elements of culture. At another level, structurally a community is found to be essentially heterogeneous, its members speaking many languages, having different cultural traits and various morphological and genetic traits, which, as mentioned earlier, are reported to be on a larger scale within a community than between communities.

Indian society is marked by division. There are no communities without divisions. On the face of it, segments (including exogamous divisions, groups and subgroups), synonyms, surnames and titles add up to a mind-boggling figure of about 80,000. However, at another level they form a fascinating tapestry marked by different levels of

perceptions, identity and status. They also demonstrate a wide range of interaction and sharing, of linkages and commonalities, among communities in a linguistic-regional context.

Each region—and even a few of the sub-regions—has its own cluster of communities, and its own hierarchy of *jatis*. All communities are placed in a hierarchical order. Based on self-perception and others' perception, the communities are now ranked as the high, the middle and the low ranks. There has been an all-pervasive impact of the development process; even though access to developmental benefits as also to market is rather uneven. As the movement towards political equality grows, and as it is translated into economic terms, there is a swelling of the middle rank. Members of more and more communities from the lower order move into the middle zone. This explains the phenomenon of the burgeoning middle class, an amorphous category which encompasses a whole range of people moving up and moving down into a growing arena of economic activities. The POI Project highlights the rise of the middle class over a large social spectrum including most communities and from almost all regions. However, there are still some communities who have no adequate representation in these ranks. Similarly, even the most remote communities have been drawn into the vortex of Indian politics, and they are participants in the political processes. However, this process has still to move forward so as to encompass all in order that our democracy—the social base of which is widening—becomes truly and fully a participative one.

Changes and diversity

None of the identities, whether in the form of communities or in the form of segments, have ever remained frozen in time and space. One need not go far into history to see how identities have evolved. One has only to compare colonial ethnography and the POI to identify the areas of change. There are five of them. Firstly, the myths of origin differ sharply. As the movement towards political equality grows, the old myths of origin marked by the notion of degradation are discarded. The current perception of origin or self-perception reflect a new sense of self-respect. Secondly, the old *varna* hierarchy seems to have collapsed or seems to be gradually replaced by the three-tier structure of high, middle and low positions. Thirdly, there has been a range of occupational diversifications within a community, breaking the old nexus between a community and its traditional occupation. Fourthly, there has been a pervasive impact of the development process. Lastly, the mutual perception and relationships of communities, particularly modern relationships, are being radically altered with political and economic change.

It should also be noted that the relationships of the main communities and their segments have been a dynamic one. The old endogamous units or *jatis* within a community or a caste have broken down, and the caste or the community has emerged as the larger endogamous unit. This is also one aspect of the consolidation of a community.

The extent of diversities existing in the country have alarmed some observers, even serious scholars, who believe that identifying—much less, studying—such diversities

will be an invitation to disaster, break up the country and society, and so on. Diversities cannot be ignored but should be observed to see how they function. Diversities are natural, native, part of our biological, linguistic and cultural heritage, and without diversities we would not have survived as a civilisation, or as a cultural system. Diversities are intrinsic not only to human evolution but also to human existence. Diversities form a pattern of their own; they have a rhythm of their own.

And yet various cultural and linguistic traits tend to coalesce in their own formations, in a manner which is natural, spontaneous and effortless. Diversities, linkages, variation of traits and their convergence—they always go together—are the components of our biological, linguistic and cultural heritage.

So much of diversity and so many of the linkages are located within the civilisational framework that the people of India have built up over centuries. Both are reflected at the cognitive levels, in different schools of philosophies. There has not only been an understanding of self amidst diversity, but also a willing acceptance of the other. Out of the objective reality of diversities has emerged an understanding of diversities, which, in spite of conflict and tension and occasional bloodbath, has generally endured. Out of this understanding of diversities has emerged a spirit of tolerance. These diversities have also flourished in a state of relative cultural freedom. Therefore, diversities go with freedom. Diversities and linkages, freedom and tolerance go together.

Effects of economic globalisation

A question that arises is whether the cultural diversities will survive or whether they will go away with the globalisation of economy. A high priest of economic globalisation recently observed in Delhi that while the economy is being globalised, governance remains national, and culture continues to be local and ethnic. There are fears not only in the developing countries about western hegemonisation of indigenous cultures, but also in some sections of the people in the developed countries about the possible impact of economic globalisation on cultural homogenisation. The question, therefore, that is being asked everywhere is whether culture, like economy, will also become globalised or homogenised. The answer to this question lies in the understanding of culture. If we take a long-term view of culture and see culture as a river that absorbs many streams and flows on, then we shall be able to take a balanced view of the changes that are likely to occur. There is no doubt that some aspects of culture like food habits, dress, music and so on which are even ordinarily more prone to change will be influenced—particularly for those who join the international circuit or those who are directly exposed to global influences. Such changes have occurred throughout history but the pace of change is much faster, almost mind-boggling, today. There are many other aspects of culture that might not experience the same impact of change, or might not change at all, for people in various age groups. In fact there is a possibility that with the perceived threat to identity, a return to the roots might be faster as one can see in the movements of the indigenous peoples or in the environmental movements all over the world.

As we observed in the beginning, we have been able to generate, under the POI, a composite profile of the people of India in its biological, cultural and linguistic

dimensions. However, the process of updating the material and generating fresh material and perspectives on change has to continue. The database has to be continually updated and enlarged to meet the requirements of our people. The Department of Biotechnology has identified a number of projects on genomic diversities. On the basis of the cultural data generated by the POI Project, efforts are now being made to explore the molecular basis of genetic variation among some of our population groups. As we have covered only 800 communities under various parameters of anthropometric and genetic surveys under the POI, it should be possible now to launch a pan-Indian survey of all populations, with the new tools of molecular biology. A second phase of the POI cultural project is also on, to analyse the traits at a natural level and in greater depth. The possibilities of a linguistic survey are being discussed, though mutedly. Language does not always divide but can serve as an instrument of integration. Language is a microcosm of many influences which are absorbed as it grows and spreads. Therefore, we may look forward to the emergence of a more composite profile of all communities of India, in the first or second decade of the next century.

References

1. Basu, Arabinda and Sreenath, J. (1995). *Anthropometric Variation in Assam, Bihar and Orissa*. Anthropological Survey of India, Calcutta.
2. Basu, Arabinda and Sreenath, J. (1996). *Anthropometric Variation in Maharashtra and Gujarat*. Anthropological Survey of India, Calcutta.
3. Ghosh, G.C. (1988). *All India Bio-Anthropological Survey: Preliminary Tables* (compiled). Anthropological Survey of India.
4. Guha, B.S. (1935). *The Racial Affinities of the People of India*. In Census of India (1931). I, India, Part III-A.
5. Risley, H.H. (1915). *The People of India*. Thacker Spink and Co., Calcutta.
6. Shree Krishan (ed.). (1990). *Linguistic Traits Across Language Boundaries: A Report on All India Linguistic Traits Survey*. Anthropological Survey of India, Calcutta.
7. Singh, K.S. (1992). *People of India: An Introduction*. Anthropological Survey of India, Seagull Publications, Calcutta.
8. Singh, K.S. and Manoharan, S. (1993). *People of India: Languages and Scripts*. Oxford University Press, Delhi. IX.
9. Singh, K.S., Bhalla, V. and Vinod Kaul. (1994). *People of India: The Biological Variation in Indian Populations*. Oxford University Press, Delhi. X.
10. Sirajuddin, S.M., Ahmad, S.H. and Singh, R.D. (1992). *The All India Anthropometric Survey, South Zone, Karnataka State (Analysis of Data)*. Anthropological Survey of India, Calcutta.
11. Sreenath, J. and Ahmad, S.H. (1989). *All India Anthropometric Survey, South Zone, Andhra Pradesh (Analysis of Data)*. Anthropological Survey of India, Calcutta.
12. Sreenath, J. and Basu, Arabinda. (1996). *Anthropometric Variations in Punjab, Haryana, Himachal Pradesh and Jammu & Kashmir*. Anthropological Survey of India, Calcutta.

10

The Indian heritage – A sociological perspective

André Béteille

Department of Sociology, University of Delhi, Delhi

A sociological perspective on the heritage of India must ensure against yielding either to a nostalgia for the past or to a wholly negative attitude towards it. There are extreme examples of both in the available literature, and it is difficult to achieve and maintain a proper balance between the two. At the height of the national movement, many Indian writers felt impelled to reconsider their own heritage and to present a picture of a pristine past in which people lived in peace and harmony with each other, and the community met the basic needs of the individual to everybody's satisfaction. This kind of nostalgia for the past is intellectually sterile, and can serve very little practical purpose in the contemporary world.

At the other extreme is the view that India's past was characterized by ignorance, superstition, oppression, exploitation and disorder, and as such there was nothing of value in it. One can find plentiful evidence of all these from the present and the recent past, and this evidence cannot be easily swept under the carpet. At the same time, it is difficult to believe that a civilisation of such wide span and historical depth could have maintained itself for two thousand years and more while negating all fundamental human values. A characteristic response to this is to say that the present and the recent past tell us less about the Indian heritage than about the subversion of it by modernisation. This intransigent hostility to modernity leads inevitably to a glorification of the past.

We cannot disregard our heritage without depriving our present identity of its meaning and significance; nor can we opt out of the modern world any more than a man can jump out of his skin. The perspective I propose to present builds on the writings of several earlier Indian anthropologists, notably Irawati Karve (1968) and N.K. Bose (1975). These scholars not only made extensive field investigations of contemporary Indian society but also examined the classical texts in order to get a better understanding of the present in the light of the past. Their view of their past was appreciative but critical, and they were acutely aware of the need to be selective in using materials from the past for constructing the future.

The modernisation of India that began with British rule has revealed the strengths as well as the weaknesses of India's social and cultural heritage. It is important to view objectively and with the maximum possible detachment both the strengths and the weaknesses, although there are no satisfactory measures of either the one or the other that will enable us to draw up an exact balance sheet. Much can be learnt by reflecting not only on the strengths but also on the weaknesses of what has come down to us from

the past. There is, no doubt, continuity of both social structure and culture, but our present goals are not identical with the ones by which life had been governed in the past, and it is beneficial to remember that what had been strengths in the past may become weaknesses in the present and *vice versa*.

Heritage of diversity

The first striking feature of India's social and cultural heritage is its diversity. It is true that India is a large country with every type of geographical environment and a very numerous population. But even for a country with its extent and population, the diversity is remarkable. There is, firstly, the great diversity in the biological composition of the population: every type of physical trait, such as height, head form, shape of nose, skin colour and even eye colour, is found in notable proportions in one group or another. At the same time, it is doubtful that any clear relationship can be established between the biodiversity of India's human population and its social and cultural diversity. And despite the enormous range of physical traits, attempts to establish a racial classification of the population have not met with any notable success.

Many anthropologists have recorded in detail the inexhaustible variety in the habits, practices and customs of the people of India. It was customary among anthropologists of an earlier generation to start with the distribution of material traits, such as food, dress, habitation and the material arts and crafts. Mrs. Karve has alluded to the endless variety in the types of food eaten and their preparation [Karve, 1968: 1]. Some of this variation, she noted, can be easily attributed to variations in the types of food grown under different geographical conditions. But these simple variations were subjected to infinite elaboration through the action of customs, conventions, rituals and other social prescriptions and interdictions whose operation has little or no connection with the known facts of geography.

Mrs. Karve made an interesting observation while recording variations in forms of dress. After pointing out that in the north, women generally wear white whereas colours are much in evidence in the south, she noted: "In Orissa the north and the south meet somewhere on the coastal plain near Kalingapattanam. In all Kalinga villages, women are dressed in white whereas, in the nearby non-Kalinga villages, women have coloured saris" [Karve, 1968: 4]. N.K. Bose devoted much time to the study of traditional crafts such as those of the oilpresser, the potter and the blacksmith [Bose, 1975: 73-86]. He noted that there was an enormous variety of techniques in each case and that differences in techniques were jealously maintained by their practitioners from generation to generation even when they lived in the same village or in adjacent villages.

Side by side, there were differences in social relations and social institutions such as those associated with family, marriage, kinship, inheritance, succession and residence. To quote Mrs. Karve again, "The variety of family organisations is equally great. Polygamy and polyandry are both found. There are groups which are matrilineal, others which are patrilineal. The taboo on consanguine marriages changes from region to region and from caste to caste . . . The modes of inheritance and succession are also different" [Karve, 1968: 4-5]. Here as well, variation may be noted not only between different regions but also within a single district and sometimes even a single village.

There is finally the inexhaustible multiplicity of religious beliefs and practices. Within Hinduism itself one can pass from the crudest worship of sticks and stones to the most profound speculation about Nature and the significance of the Universe. But Hinduism is not the only religion of India. In addition to its offshoots, Jainism and Buddhism, other religions such as Islam and Christianity have also made their home in the country. It is well to remember that there are more Muslims in India than in any other country in the world save Indonesia, and that Christianity has existed in some parts of India longer than in many European countries.

Although Islam, Christianity and other religions have an important place in contemporary Indian society, it is Hinduism that has contributed the most towards giving Indian civilisation its distinctive form and ethos. It is the oldest among the major religions of the country, and most Indians from ancient to modern times have been Hindus in one sense or another. Although Islam was the politically dominant religion in large parts of the country for several centuries, it did not absorb Hinduism or efface the basic design of Hindu social structure. Nor did Hinduism, where it was demographically and otherwise dominant, seek to eliminate the beliefs and practices characteristic of other religions. India has been and continues to be a land of many religions and religious sects, each enjoying a measure of autonomy in its own sphere. It is not uncommon to find local communities even in the rural areas in which not only Hindus with various beliefs and practices but also Muslims and Christians pursue and maintain their distinctive styles of life.

The characteristic of accommodation

The heritage of India has been built out of many components. This becomes evident when we look at its linguistic and religious diversity. New components, whether from within or outside, have been continuously accommodated throughout history. In being accommodated, these components acquired new orientations, but their old identities were not allowed to lapse. N.K. Bose provided an outstanding account of the Hindu method of tribal absorption [Bose, 1941] which applies by and large to the accommodation of all kinds of social formations, tribal as well as non-tribal, from within and outside the country.

Accommodation without assimilation has been the characteristic of Indian civilisation until modern times. This has enabled the co-existence of a large multiplicity not only of beliefs and practices but also of collective identities. Adding new components has not meant discarding old ones, so that new and old components of the most heterogeneous kinds have existed cheek-by-jowl to a far greater extent than in other civilisations. Mrs. Karve has put it thus: "The historical process is one of continuous accretion. There does not seem to be a stage where a choice was made between alternatives, a choice involving acceptance of one alternative and a definite, final rejection of the others" [Karve, 1968: 7]. One can say in this light that Indian civilisation has not been the outcome of a single, consistent or exclusive ideology; the accommodation of diversity has been its underlying ideology.

The presence of diversity has been more than a matter of mere existence. Here, according to most authorities, a decisive part has been played by the core values of Hinduism in shaping not only Hindu society specifically but Indian society as a whole.

Respect for the diversity of habits, customs and practices was enjoined not only by Hindu religion but also by Hindu law. There is a maxim of *Yagnyavalka* that says that one should not practise that which, though ordained by the *Smṛiti*, is condemned by the people [Kuppuswami, 1991: 44]. P.V. Kane's monumental *History of Dharmasastra* gives a vivid account of the extraordinary maze of law, custom and usage by which social life was regulated in the past. *Deshachar* or the customs of the locality and *lokachar* or the customs of the community generally prevailed over what was prescribed by the *shastras*.

Bose examined in detail the implications for the structure of society of the primacy of custom and usage over codified law. Society came to be divided into innumerable tribes, castes, subcastes, clans, sects and communities, each of which sought jealously to maintain its own style of life and its own code of conduct. The classical and medieval authorities sought again and again to fit the multitude of actually-existing groups into the four-fold scheme of *varnas*, but their efforts were never wholly successful. At all times there were groups that existed on the margins of the four-fold division, or in its interstices, or beyond the pale. The establishment of Muslim rule over large parts of the country added to the inventory of groups and at the same time made it more difficult to fit them into the scheme of *varnas*.

The polymorphous structure of Hindu society and its pluralist, not to say polytheist, cultural tradition provide congenial conditions for the growth of democracy. Democracy favours a diversity of ends and is averse to a single plan of life for everyone; it supports a plurality of parties and interest groups and opposes the control of society and politics by one single group or type of group. In short, the building of democratic institutions in modern India is likely to benefit from its long tradition of diversity and accommodation in social and cultural life.

Hierarchy in organisation

Having taken note of the remarkable accommodation of diversity in traditional India, it is now necessary to ask how this diversity was held together and organised. To put it in a nutshell, its organisation was hierarchical and not democratic. Much has been said about democracy in ancient India, but little of it will stand up to careful scientific scrutiny. The Indian village has been described time and again as a little republic, but the plain fact is that such unity as it had in the past was a hierarchical unity in which the upper castes owned or controlled the land and the untouchables provided servile or semi-servile labour, with all kinds of grades or ranks in between [Béteille, 1980].

Most modern authorities would acknowledge that India's plural society had a hierarchical structure. Some would lay stress on the plurality and others on the hierarchy, but it is important to keep both in mind. Traditional India has been widely regarded as the prototype of a hierarchical society [Dumont, 1966; Béteille, 1987], and the marks of hierarchy are readily visible in its contemporary structure. While styles of life of the widest variety were acknowledged and accommodated, they were not all equally esteemed. An elaborate ritual idiom served to express social distinctions between superiors and inferiors. Not only was each group expected to persevere in its own style

of life, but there were sanctions against the adoption by groups of inferior rank of the symbols of status allowed to their superiors. The law of the *Dharmashastra* noted in detail the privileges and disabilities of groups in keeping with the positions they occupied in society.

From whichever angle we view the case, the modern principle of equality was largely absent in traditional Indian society. True enough, equality was acknowledged on the metaphysical plane, but it had hardly any place on the plane of everyday social and political existence. Now law and politics have both changed. They presuppose a certain basic equality among persons; but the practice of inequality remains deeply embedded in every sphere of Indian society.

Just as the accommodation of diversity did not go with equality in the traditional order, it also did not go with individual freedom. Now, it is a characteristic of hierarchical societies in general that collective identities prevail over individual identities, and this characteristic was developed in its fullest form in traditional Indian society [Tocqueville, 1956; B  teille, 1987]. Speaking of village, caste and joint family as the fundamental institutions of traditional Indian society, Nehru had observed, "In all these three it is the group that counts: the individual has a secondary place" [Nehru, 1961: 248]. Individual freedom could of course be asserted by renouncing society and adopting the way of the *sanyasi*; but even here, *sanyasis* in course of time became organised into groups of various kinds.

Thus, while a great variety of occupational techniques, marriage practices and ritual procedures were present in society as a whole, no individual could choose from among these according to his own inclination or convenience. The actions of the individual were severely constrained by the rules and practices of the group into which he was born. India has been described as "a land of . . . the most inviolable organisation by birth" [Weber, 1958: 3], and here too the spirit of the old social order was antithetical to the spirit of democracy.

It has been noted over and over again that India's continuity as a civilisation was social and cultural rather than political: order and stability were maintained not by means of the state but through a peculiar balance of social morphology and cultural values [Baechler, 1988]. In this view, the state was weak and transient whereas culture and society were cohesive and enduring. Today it is not altogether clear how effectively order and stability were in fact maintained in past times. The authorities prescribed rules of conduct of such complexity that it is doubtful that any real society could ever be regulated by them. The classical authorities convey a strong sense of living in times of great disorder together with their obsessive preoccupation with rules. Perhaps this pervasive sense of disorder and the urge to prescribe the most detailed rules of conduct were two sides of the same coin.

What is clear is that the old principles by which society has been governed for two thousand years and more are no longer adequate for maintaining either order or stability under modern conditions. Whatever may have been the degree of disorder and instability at particular times and particular places, both inequality of status and the subordination of the individual to the group were, generally speaking, morally acceptable principles in the past. Such is no longer the case. The challenge today is to maintain the diversity

and the spirit of accommodation inherited from the past while repudiating hierarchy and creating more space for individual freedom.

Classical India and the Constitution of India

Today Indian society is characterised not only by diversity but also by conflicts of various sorts. Among these I will point only to the conflict of norms and values. By values I mean the generalised ends that are culturally prescribed or at least considered desirable; by norms I mean the regulatory rules by which conduct is governed in society.* Here, there are pervasive conflicts between the norms and values inherited from the past and those regarded as appropriate to the modern world. The normative order of classical India, its design so to say, may be found in the *Dharmashastra*, and in particular in the *Manusmriti*; the normative order of modern India is encoded in its Constitution. There is a striking discordance between the two.

The generalised ends considered desirable in the past have not entirely lost their salience, but new ends have now come into view. Today equality in social life has acquired a certain appeal among persons in many walks of life; but the commitment to hierarchy that marked the traditional order is still widely manifest beneath the surface. Recognition of the autonomy of the individual and the respect due to him or her is now an important value; it is at odds with the strong sense of obligation to the group of which one is a member by birth.

Diversity on the plane of values or generalised ends is to be expected in any large society undergoing a major transformation, and its tolerance is healthy upto a point. But how far can a modern society accommodate a plurality of norms or regulatory rules that are not only diverse but also unclear, ambiguous and mutually inconsistent? Whereas the diversity of generalised ends is diffused through society as a whole, the contradictions among the regulatory rules manifest themselves most clearly in particular institutional domains. There is widespread anxiety today over the many problems with which public institutions are beset: misuse of funds, lack of discipline, absenteeism, work stoppages, strikes, and so on. All of these are related in one way or another to the failure of regulatory rules. Allegations about the violation of rules have become endemic, and they lead to the creation of new rules which are in turn violated.

The proliferation and disregard of rules

I would like to conclude by drawing attention to two striking features of contemporary Indian society that manifest themselves in all public institutions from the State downwards. The first is the drive to create rules of every kind and to the last detail; and the second is the wide disregard of those very rules. My view is that the proliferation of rules and the disregard of rules are two sides of the same coin; and, further, that these two complementary tendencies are both very deeply rooted in India's traditional culture.

Citizens the world over complain about the obstacles created by the multiplicity of rules they have to face in their dealings with any branch of the government, but the

problem is particularly acute in India. In our government offices, rules are used as weapons of offence and defence, and every official and his clerk is equipped with an inexhaustible armoury of them. Part of this is the wilful display of authority by the man sitting on an official chair, but there is more to it than that. In the Indian case the rules themselves are numerous, complex and ambiguous; this can be checked by looking at rules in comparable systems elsewhere. Even when an official wishes to be helpful or expeditious, he is kept in check by the jungle of rules endemic to our way of administration.

I would like to stress that I am dealing with a tendency that is deeply rooted in our culture, and not simply with the malfunctioning of governmental bureaucracy. The jungle of rules is all-pervasive and we can examine how it works in universities, hospitals and many other institutions that have no direct connection with the government. I shall take the example of universities since I have direct personal knowledge of their functioning. Nowhere in the world is the work of universities obstructed by so many rules; and nowhere in the world are the rules relating to academic work so extensively violated. There are many thoughtful and well-intentioned scholars who are aware of this and disturbed by it; but they seem unable to do very much about it. Committees set up to streamline procedures invariably create new rules, and then Mrs. Karve's law comes into operation; the addition of new rules does not lead to the elimination of old ones; those are simply put into cold storage, to be taken out when required to trip up an unwary newcomer who tries to put some dynamism into the system.

I have come to the conclusion that we have an orientation towards rules that is largely our own and that is strikingly different from the orientations characteristic of other cultures. Bankimchandra, the great 19th century Bengali writer, was troubled by the tendency of some of his contemporaries to quote prescriptions from the *shastras* to support one or another reform they wished to promote. He found those prescriptions to be prolix, ambiguous and self-contradictory. He wrote, "Indeed, it is not possible for any society to be fully regulated by all the prescriptions to be found in the *shastras* of Manu and the others. It is doubtful if ever, at any time, those prescriptions were fully operative in any society. Many of them are inoperable. Many, though operable, involve such hardships to man that they would drop out on their own. Many are mutually contradictory. If any society is ever destined to keep all these prescriptions in operation, such a society must indeed have an evil destiny" [Bankimchandra, 1975: 316]. Those who are frustrated by the jungle of rules in offices in modern India may secure some consolation from Bankim's reflections on the past.

How do people get things done in the face of this plethora of obsolete, unclear and inconsistent rules? They improvise, activate personal networks, and go about their business without paying too much attention to the rules. This probably is how they worked the system in the past, and this is how they try to work it today. But people lived largely in small, face-to-face communities in the past. They now operate in a world that is organised in a very different way and on a very different scale. Is it possible to act effectively in the modern world without a radical change of orientation towards the regulatory rules of society?

References

1. Baechler, Jean. (1988). *La solution Indienne*. PUF, Paris.
2. Bankimchandra. (1975). *Bankim Rachanabali* (in Bengali). Sahitya Samsad, Calcutta. 2.
3. Bêteille, André. (1980). The Indian Villages: Past and Present. In E.J. Hobsbawm, K.N. Raj and I. Sachs (eds.) *The Peasant in History: Essays in Honour of Daniel Thorner*. Oxford University Press, Calcutta.
4. Bêteille, André. (1987). *The Idea of Natural Inequality and Other Essays*. 2nd edn. Oxford University Press, Delhi.
5. Bose, N.K. (1941). The Hindu Method of Tribal Absorption. *Science and Culture*. VII, 188–194.
6. Bose, N.K. (1975). *The Structure of Hindu Society* (translated from the Bengali with an introduction and notes by André Bêteille). Orient Longman, New Delhi.
7. Dumont, Louis. (1966). *Homo hierarchicus*. Gallimard, Paris.
8. Karve, Irawati. (1968). *Hindu Society: An Interpretation*. 2nd edn. Deshmukh Prakashan, Poona.
9. Kuppaswami, Alladi (ed). (1991). *Mayne's Treatise on Hindu Law and Usage*. 13th edn. Bharat Law House, New Delhi.
10. Nehru, Jawaharlal. (1961). *The Discovery of India*. Asia Publishing House, Bombay.
11. Tocqueville, Alexis de. (1956). *Democracy in America*. 2 vols. Alfred Knopf, New York.
12. Weber, Max. (1958). *The Religion of India: Hinduism and Buddhism*. The Free Press, New York.

11

The language heritage of India

D. P. Pattanayak

Formerly, Director, Central Institute of Indian Languages

The development of humans is characterised by brain size and the ability to speak. Every child is born with the ability to speak, but whether in Tamil or Hindi is a historical accident. Speaking is not merely for communication; it is used to convey thoughts and is an important factor in human group formation. Indian language heritage, therefore, dates back to the earliest humans found in India. Anthropologists have posited a negroid substratum which is all but lost in India but some traces of negroid features can be found in some of the tribals of India. The Austrasiatic, the Dravidian and the Indo-European are the major language families in India. India has a Sino-Tibetan reign in the north and northeastern border which constitutes the fourth type. With the dispersal of the Tibetan population all over the country, the Sino-Tibetan language has begun to come in contact with the other three languages. It is said that language is a barrier to convergence. I give here two examples to disprove this. In India we have three tongues: one is known as Nagami and is used all over the northeast, another is Sadari which is a common language among Oriya, Bengali and Hindi speakers, and the third is Desiya which is a common language among the tribals along the Andhra-Orissa border. And that is the language they use to communicate with both the Oriyas as well as the Andhraites. Therefore I want to clarify that language is not a barrier to convergence. The second example that I want to give is that from a study of a village called Kupwa which is located on the Maharashtra-Karnataka border. There are three languages spoken in that area—Marathi, Kannada and Urdu—all of which operate simultaneously. Therefore, there are mechanisms which people use to communicate with one another in any of the three, with equal facility.

Indian scientists are embarking upon a study of genome diversity to see what these communities are about. India is home to 4,694 communities including 75 endangered tribal groups, speaking 1652 mother tongues, as given by the census of 1961, approximating to 324 languages, by a range of castes or caste complexes and not single castes. Ramanuja converted lower castes into Brahmins. There are Mali Brahmins, Aranyakas, cultivating Brahmins, etc. Kashmiri Brahmins eat goat's meat, and Bengali Brahmins eat fish while South Indian Brahmins are vegetarians. Iyengars and Iyers, Sarajufarias and Kanyakubjis represent another dimension. Unless one is aware of these, it is hard to pick up a Brahmin group for experimental purposes. How centuries of culture have obliterated structures beyond recognition! A debate about tumbling procedures is necessary before a study of this magnitude is undertaken.

The earliest Indian civilisation known so far is the Mohenjodaro-Harappa civilisation. The Harappan script is yet to be deciphered. The contemporary conclusion is that it is a Dravidian script and the language is Dravidian. A Finnish group, an American group and some Indian scholars support this claim. This is in contradiction to the views of S.R. Rao and Krishna Rao who support the Indo-Aryan claim.

Mahadevan in his article, *An Encyclopedia of the Indus Script*, looks into various things and quotes: "... it looks most unlikely that the Indus script will ever be deciphered, unless some radically different source material becomes available. That, however, must not deter us from trying." The Dravidian hypothesis raises more questions than it clarifies. It is believed by many that the caste structure is primarily Aryan. The question is whether a complex system like the caste structure would develop in a Dravidian civilisation or among some other regions. If the Aryans followed the Dravidians and they knew each other in their pre-Indian habitat, then it is possible that they appropriated the Dravidian structure. It is quite evident that the Dravidians came from outside. The migration maps of the world say that if there is concentration of a group and traces of the family and languages spoken by them, then it indicates the directionality of their movement. The persistent survival of Brahui, a Dravidian language, in Baluchistan and parts of Afghanistan and Iran is an important marker of the movement of the Dravidians. This also marks the Mohenjodaro-Harappa civilisation as Dravidian and indicates subsequent movement of the Dravidians to the South.

The Dravidians who came in contact with the Austrics absorbed some of their linguistic features, at the same time donating to the Austrics some features of their own. In any case, the Austrics were pushed into inhospitable areas. The Aryan pressure consolidated the Dravidians in the southern parts of the region. India has been a multi-lingual and multi-cultural country ever since its known history. It is not a post-colonial phenomenon as some assume it to be. Multiple gods and goddesses have baffled outsiders. "*Tasmai Devaya Havishabhidema*" (of these gods we think of in our rites and penances) is the expression of the bewildered Indian minds in the face of 330 million gods and goddesses. Added to this, with 4000 castes and communities and an approximately equal number of faiths and beliefs, 46,000 species of plants, and 65,000 species of animals, India presents a diversity not found anywhere else in the world.

During the historical period, Arabs, Persians, Greeks, French, Dutch, Jewish, Portuguese and others came to India and left behind their accounts about the culture of India. Muslims and Christians brought their religions also, which became indigenous. Now there are approximately 100 Muslim and 70 Christian groups in India. Both Muslims and Christians have adopted Indian languages, even for their ritual purposes. The Christian Missionary has taken leads in translating the Bible and other tracts into the vernacular languages ever since they came. During the last two decades the Koran has been translated into major Indian languages. The Muslims speak Malayalam in Kerala, Oriya in Orissa, Bengali in Bengal, Assamese in Assam and Gujarati in Gujarat. An entire language called Urdu was born out of such intercourses.

Sanskrit is the root of Indian culture. Philosophy, literature, art, sciences, engineering, medicine, surgery, archaeology and architecture—in short, the entire cultural inheritance of India—is embedded in Sanskrit. Sanskrit is our window to the world. The discovery

of Sanskrit as the binding force of Indo-European history revolutionises not only language research but also research in sociology, anthropology and political science. Lehn White Junior, writing in the *American Historical Review*, observed that the Indian concept of perpetual motion not only helped European engineers to generalise their concept of mechanical power, but also provoked a thinking by analogy that profoundly influenced Western scientific views. It is not only in the field of engineering but also in the fundamental discovery of zero, and the delineation of the decimal system, that the Indians have made such a significant impact that the Arabs referred to mathematics as Indian art. Sanskrit is also a window to India. Apart from modern Indian languages developing from a spoken counterpart of standardized Sanskrit, it is responsible for making India a single linguistic, socio-linguistic and semantic unit. Books on medicine written as early as the second century and those on surgery written in the fourth century impart a respectability to the discipline, the scholar and the Sanskrit language. Sanskrit is essential for disciplines such as philosophy, Indian history and culture, Indian archaeology, numismatics, economics and political science on the one hand and physical sciences, engineering and medicine on the other. Yet there is plenty of discussion about this in the academia. There is continuing argument about either compulsory or optional study of Sanskrit within the three language formula. Because of this the study of Sanskrit is declining in India.

English is one of our cultural heritages. It is important to note that, like Chinese and Hindi, English encompasses many languages. A decade ago, scholars were speaking of the English language. Now they are speaking about the Englishes of the world. In India, one can find varieties of English influenced by different vernacular languages. English occupies a position disproportionate to its importance in India. It is not only the associate official language of India but it has become the State official language in many of the states in northeastern India. Its growing importance as the medium of instruction in higher education, percolating to the level of play-schools, would pit it into instant conflict with modern Indian languages. As the dominant medium of communication of the elite, euphemistically called mass communication, it became an enemy of the other Indian languages. English as a supplement to other Indian languages is a strength whereas, as a substitute, it is debilitating. The manner in which it surreptitiously challenges Indian languages is alarming.

For instance it is generally taken for granted that science and technology cannot be taught through the medium of Indian languages. That is why in the Kendriya and Navodaya Vidyalayas, science and technology are taught through the English medium. I am reminded of Professor Satyen Bose who once remarked that if a Bengali cannot teach physics in his mother tongue, it is not because he does not know Bengali but because he does not know physics. The science teachers do not distinguish between concepts and technical terms and hide behind the technical terms when they fail to explain a concept. Another interesting example is provided by the following episode. Given 13 red and blue balls, how does one teach the concept of sets? The teacher said, "Keep the red ones on one side and the blue ones on the other side and it is easy to demonstrate sets." When confronted with the question of what would happen if all 13 were partially red and partially blue, she had no answer. It never occurred to the teacher

that without understanding the language it would be difficult, if not impossible, to explain. Teaching of arithmetics provides yet another example. A professor visited an English medium school and was dismayed to find the children chanting, "Two into two (2×2) is four." He said two into two is one. It was the turn of the teacher to be dismayed. The visitor said that, in English, 'into', stands for 'is divided by' and therefore in English, two into two ($2/2$) is one. If the Indian teacher interprets 'into' as 'is multiplied by', he knows neither English nor the Indian system which says "two times two is four". The teacher who swears by the universality of science forgets that technology is culture-friendly. Appropriate technology results from interaction of science with society. Science cannot interact with society through a language alien to that society. Therefore, science and technology cannot flourish in a country where English or a colonial language is given priority over its own language.

Early introduction of English as the medium of study promotes alienation to one's culture and curbs creativity. Due to inefficient teaching and learning of English and the neglect of the mother tongue, children become inefficient communicators in both languages. The Hindi folk say, "*Kuch padha, kaam choda; aur padha, gaon choda; zyada padha, desh choda*", aptly summarising the predicament of the English education. It would be clear by now that although India has a science policy and an industrial policy, it does not have a language policy. That is why the new education policy of 1986 refers us back to the three language formula of 1968. The three language formula can at best be a strategy for learning languages at the secondary stage. It certainly cannot be the substitute for a policy. National integration or joining the mainstream are terms and phrases for assimilation. For the last fifty years I have been searching for the mainstream; I am yet to find it! English seemingly pasted over the entire system produces people who are semi-lingual and incompetent, in both English and their own language. The usage of so many languages represents the rich cultural heritage of the country. Although the European Union has begun to operate with nine languages, individual heritage must be sustained and transmitted. In the absence of any effort in this direction, the Indian languages face the danger of becoming extinct. A look at the heritage of India is sufficient to show that prior to the British rule, India was never a single political entity, but it always was a single cultural entity. Travellers have eulogised India and underlined its cultural unity. This tension between its political identity and its cultural ideology helped preserve its multiplicity and diversity. Be it linguistic, cultural, religious or communal convictions, India may not have been a nation in the European sense of the term but developed as a single cultural one.

Gandhi was one of the few politicians who knew the pulse of India and said that "India lives in its five lakh villages." Karl Marx considered villages as impediments to development. Ambedkar, the chief architect of the Indian Constitution had equally bizarre views about villages. In his speech in the Constituent Assembly on 4th November 1948 he said, "No doubt the village community has lasted where nothing else lasts, but mere survival has no value. What is a village but a stink of localism, a den of ignorance, narrow-mindedness and communalism." The mindset of the leaders of the time is seen from the letter of Jawaharlal Nehru of 9th October 1945 in response to Gandhi's letter of 5th October 1945 wherein he (Nehru) says, "A village is backward intellectually and

culturally and no progress can be made from a backward environment. Narrow-minded people are much more likely to be untruthful." It is no wonder that Gandhi's *Gram Swaraj* and Lohia's Four-pillar State were drowned in the cacophony created by those who wanted to build the Indian nation in the image of their colonial masters. Builders of the developed countries have under-perceived the consequences of imposition of a single language on a bi- or multi-lingual country. Bangladesh, Pakistan, Yugoslavia and Canada are examples from which no lessons have been learnt. To take one example, Jinnah's insensitivity to the sentiments of the Bengalis, his Urdu myopia and his accent on a mono-lingual state resulted in the division of Pakistan and creation of Bangladesh. Those who talk of globalization should understand that this does not make sense without reference to localisation, and vice versa. It is unfortunate that even though educationists accept the existence of local history, regional history, national history and international history, they are unwilling to accept the presence of the languages of intimate communities, proximate communities and those of different communities. How can one talk about heritage without accepting grass root realities? The grass root reality is that one gets connected wherever one goes. If one draws a straight line from the North to the South or from the East to the West and makes a mark every ten miles, then one can see that there is no break in communication between adjacent points, but communication breaks down at distant points on the scale. Our heritage is a country which is multi-lingual, multi-ethnic and multi-cultural. Our planning must begin by accepting the grass root multi-lingualism as the starting point. Unfortunately, the developed countries have accepted multi-culturalism but they do not accept multi-lingualism. For the developed countries, one language is the norm, two languages are a quantum jump, three languages are barely tolerable and more than three is absurd. For the multi-lingual world, the existence of many languages is a fact of life. Any restriction on the choice of language use is painful. For us, three languages are tolerable and one language is absurd. To relate modernity to heritage is to link change with continuity. So far we have missed the bus. Let us hope that good sense will prevail at least now.

12

Peopling of India

Madhav Gadgil, N.V. Joshi
Centre for Ecological Sciences
Indian Institute of Science, Bangalore

U.V. Shambu Prasad
Centre for Research in Indo-Bangladesh Relations
Jodhpur Park, Calcutta

S. Manoharan, Suresh Patil
Anthropological Survey of India
Southern Regional Centre, Mysore

Abstract

We examine the demographic history of India on the basis of a new investigation of mitochondrial DNA base sequences of 101 Indians, in light of the recent synthesis of global genetic history of humans by Cavalli-Sforza and co-workers. To this population genetic evidence we add fresh insights into linguistic and anthropological patterns based on the People of India Project of the Anthropological Survey of India, and a review of the pertinent archaeological evidence on waves of diffusion of technological innovations over the subcontinent. The Indian subcontinent has been populated by a series of migrations propelled by significant technological innovations outside India since the first major expansion of non-African *Homo sapiens*, probably around 65,000 years before present (BP). The likely major migrations include (i) Austric language speakers soon after 65,000 years BP, probably from the northeast; (ii) Dravidian speakers around 6,000 years BP from the mideast with knowledge of cultivation of crops like wheat, and domestication of animals like cattle, sheep and goats; (iii) Indo-European speakers in several waves after 4000 years BP with control over horses and knowledge of iron technology; and (iv) Sino-Tibetan speakers in several waves after 6000 years BP with knowledge of rice cultivation. A notable feature of Indian society is the persistence of thousands of tribe-like endogamous groups in a complex agrarian and now industrial society. In this society, populations of dominant groups have continued to grow, while those of subjugated groups may have stagnated most of the time.

Introduction

India is a country remarkable for its diversity, both biological and human. The biological diversity owes itself to the country's position at the trijunction of the African, the northern Eurasian and the Oriental realm, its great variety of environmental regimes, and its relative stability of biological production. It is this biological wealth that has attracted to the subcontinent many streams of people at different times, from different directions, bringing together a great diversity of human genes and human cultures. While in other lands the dominant human cultures have tended to absorb or eliminate others, the tendency in India has been to isolate and subjugate the subordinated cultures, thereby

augmenting cultural diversity. This tendency to nurture diversity has been favoured by the diversity of the country's ecological regimes [Gadgil and Guha, 1992].

People migrate because of pulls from their destination and pushes in their homeland, often propelled along by some technological advantage. Thus in the 16th century, Europeans came to India in search of spices, pushed out by the Little Ice Age that had gripped Europe, equipped with superior sea-going vessels and guns. That migration is well documented and understood; but it is the many earlier ones that have brought to India the bulk of human genes and cultural traits. It is our purpose in this paper to elucidate what we can, of these earlier migrations.

Role of innovations

People have of course migrated out of India as well, but these out-migrations have been on a much smaller scale, and mostly over the last three centuries. This is related to the fact that India has never been the site of any significant technological innovations. A series of important innovations have, over the years, taken place outside India—innovations which have given an edge to people in control of these innovations, propelling major migrations [Habib, 1992].

In chronological order, the most relevant of these include: (i) evolution of symbolic language, probably by the first modern *Homo sapiens*, in Africa, perhaps around 100 kybp (kybp = thousand years before present); (ii) husbanding of wheat, barley, cattle, pig, etc. in the mideast around 10 kybp; (iii) husbanding of rice, buffalo, etc. in China and Southeast Asia around 8 kybp; (iv) domestication of the horse in Central Asia around 6 kybp; (v) use of iron in Anatolia around 5 kybp; (vi) use of stirrups for horse riding in Central Asia around 2 kybp; (vii) use of gunpowder in China around 2 kybp; (viii) use of cannons and guns in war in Arabia in the 15th century.

Our theme then is that these manifold innovations to the west, east and north of the Indian subcontinent have propelled many waves of people into our land, giving rise to what is genetically as well as culturally the most diverse society in the world. There are diverse lines of evidence for these migrations—genetic, linguistic, archaeological, and anthropological. We will endeavour to draw on all these disciplines to reconstruct the story of the peopling of India.

Genetic affinities

Genetically and culturally, India is perhaps the most diverse country on the face of the Earth. The most authoritative summary of the genetics of human populations is provided by Cavalli-Sforza in his magnum opus, *History and Geography of Human Genes* [Cavalli-Sforza et al., 1994]. He provides global maps of frequencies of 82 genes for 42 population aggregates of indigenous people covering the entire world. The 82 loci show the highest levels of heterozygosity (0.35–0.37) for northwestern India, West Asia and continental Europe (Fig. 1). Parts of southern and eastern India share slightly lower levels of 0.33–0.35 with western China, Central Asia, Scandinavia and northern Africa. The lowest levels of 0.21–0.23 occur in New Guinea and western Australia. Such genetic data is

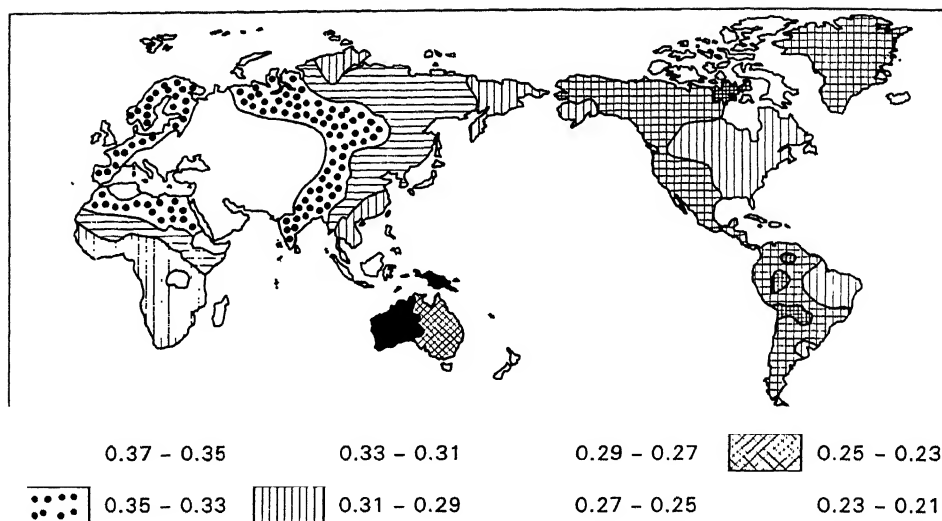


Fig. 1 Global distribution of mean genetic heterozygosity of indigenous populations based on frequencies of 82 genes for 42 world population aggregates [Cavalli-Sforza et al., 1994]

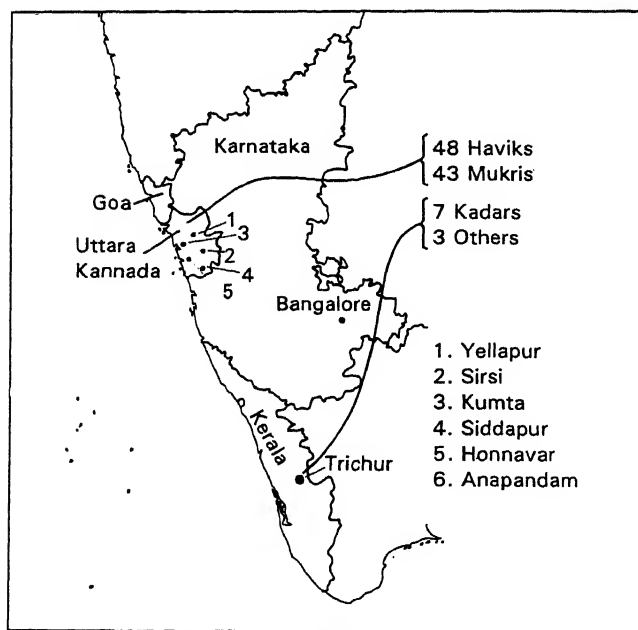


Fig. 2 Geographical location of collection of genetic material from Havik (48), Mukri (43) and 7 Kadar populations in the South Indian states of Karnataka and Kerala [Mountain et al., 1995]

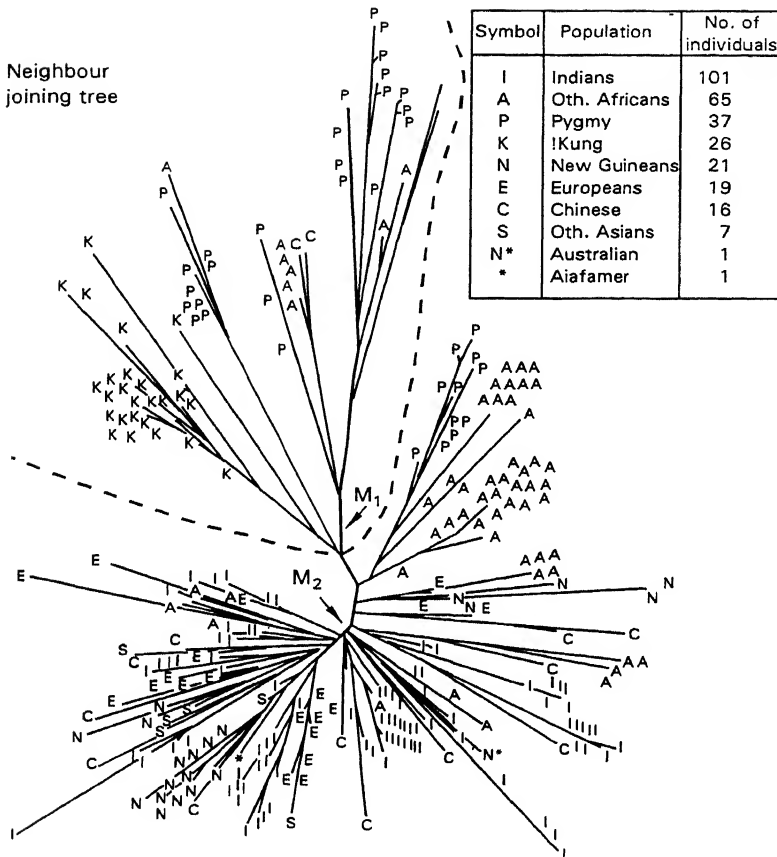


Fig. 3 Neighbour joining tree based on 745 mitochondrial DNA sequences from 101 Indians, 36 Pygmies, 26 !Kung, 65 Other Africans, 21 New Guineans, 19 Europeans, 16 Chinese, 7 Other Asians, 1 Australian and 1 Afro-American [Mountain et al., 1995]

however rather limited, based on traditional markers such as blood groups. Modern genetic techniques have greatly added to the wealth of genetic information that may be obtained from a single individual by looking at the nucleotide base sequences of DNA molecules themselves. The most variable of such sequences occur in two hypervariable regions of mitochondria, which are purely maternally inherited in humans. We have collaborated with Cavalli-Sforza and his colleagues of the Stanford Medical School to examine the DNA sequences of 791 base pair lengths from the D-loop region of mtDNA for 101 Indians [Mountain et al., 1995]. Of these, 48 belonged to the upper caste Havik group and 43 to the scheduled caste group of Mukris from the coastal Uttara Kannada

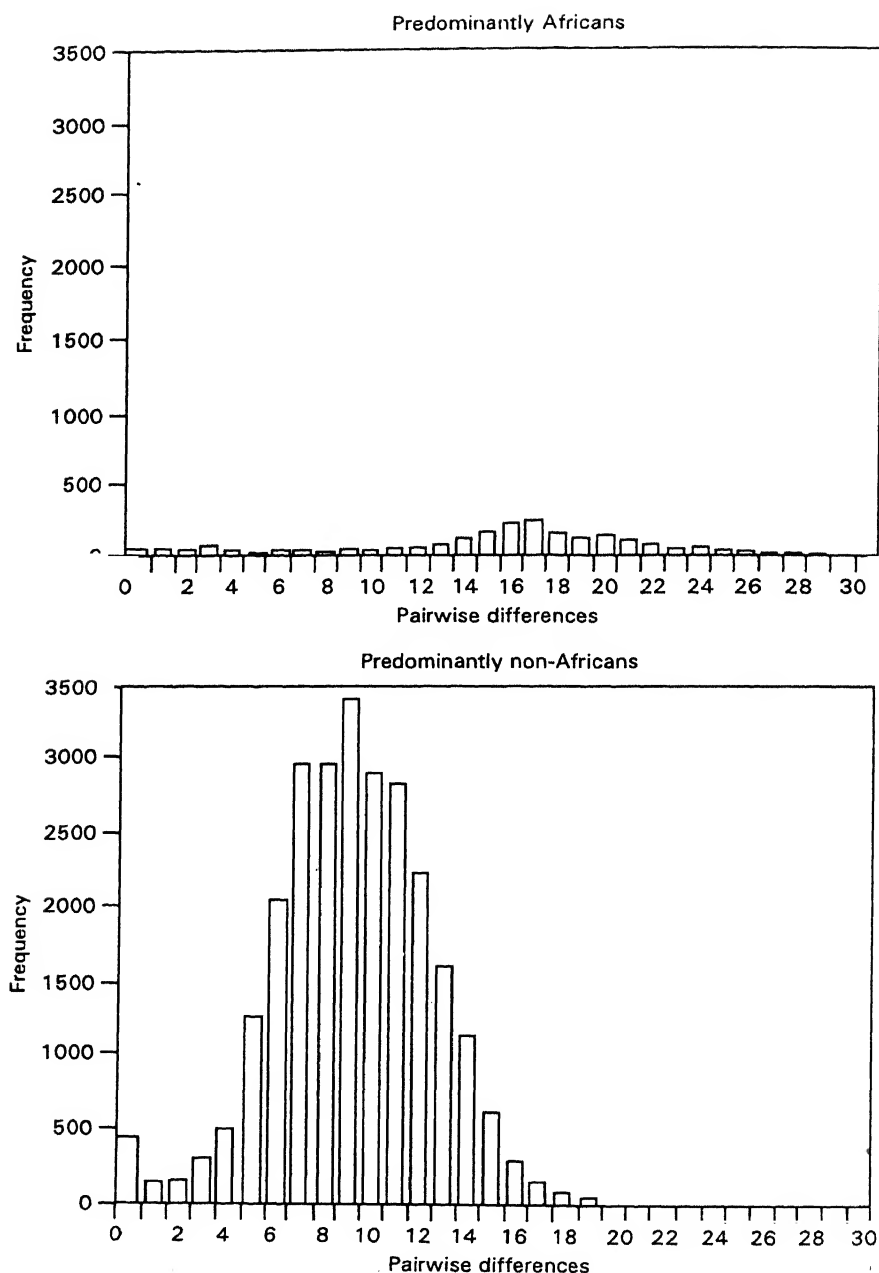


Fig. 4 Distribution of pairwise differences in the 745 mitochondrial DNA base pair sequences for the 65 sequences rooted at M_1 and 229 sequences rooted at M_2 for the neighbour joining tree depicted in Fig. 3 [Mountain et al., 1995]

region of Karnataka, 7 to a tribal population called Kadars from Kerala, and 3 to other Indians involved in field collection of samples of scrapings of cheek cells and scalp hair roots (Fig. 2). Eighty-six of these 791 sites demonstrated some variation amongst Indians; it was also possible to compare 745 from amongst these 791 sites with published data on 187 individuals from Africa, Europe, China and other parts of Asia along with one Australian and one Afro-American individual [Vigilant et al., 1991]. Figure 3 is a neighbour joining tree based on this genetic data on 294 individuals. The tree has two distinct trunks rooted in M_1 and M_2 . The first trunk includes 65 sequences: all !Kung, most Pygmies, 10 Other Africans and two Chinese; the second trunk includes 229 sequences including 11 Pygmies, 55 Other Africans and all the non-Africans with the exception of the two Chinese. It is evident then that the primary genetic differentiation of the human species is between Africans and non-Africans, with Indians intermingling with Europeans and Chinese.

The magnitude of base pair differences in these sequences can permit us to estimate the time elapsed since common ancestry. Figure 4 presents such a distribution for the two trunks of the phylogenetic tree. Evidently the group of 65 (predominantly Africans) with a mode around 17 are far more diversified genetically than the 229 primarily non-African sequences with a mode around 10. The time estimated to have elapsed since common ancestry of course depends on the mutation rate, which is probably somewhere between 1 in 100,000 to 1 in million for this hypervariable region of mtDNA. That gives us a range of 22 to 220 kybp for the first and 13.6 to 136 kybp for the second trunk. This is in conformity with the current view that modern *Homo sapiens* populations underwent a first expansion within Africa around 100 kybp, and a second expansion outside Africa around 65 kybp. The *Homo sapiens* peopling India are then a part of this second expansion—an expansion that may have occurred in southern China [Ballinger et al., 1992] or in or close to the Indian subcontinent itself [Mountain et al., 1995].

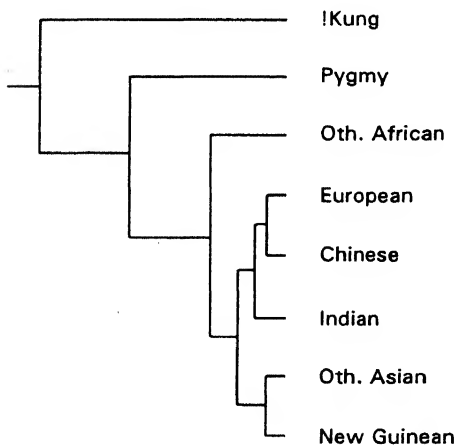


Fig. 5 Dendrogram inferred according to average linkage algorithm based on simple genetic distances amongst the major population groups [Mountain et al., 1995]

This data can also be used to construct a tree summarising the relationship amongst the major human groups (Fig. 5). As expected, this tree separates out Africans from non-Africans. Among the non-Africans, the Europeans, Chinese and Indians are almost equally close to each other, being a little more separated from other Asians and New Guineans. The Indian population of today might then be surmised to have been put together by many ebbs and flows of people over the huge Eurasian continent.

Gene analysis reveals people radiating out of the Middle East and the Orient

To assess the patterns of these ebbs and flows, Cavalli-Sforza et al. (1994) have examined the frequencies of 69 genes from 42 populations covering all of Asia. Any given population is then represented as a point in the 69-dimensional space. This information can be summarised with the help of a multivariate analysis technique called principal components (PCs). The first PC for Asia explains 35.1% of the total variation in the gene frequency; the second PC explains 17.7% of the variation (Figs. 6 and 7). Subsequent components explain relatively little. These two maps are most instructive. The first PC map suggests that genetic affinities amongst Asian populations decline with distance along an East–West axis. This is compatible with movements of people radially fanning out from the Middle East, although it could also result from a westward movement along a very broad front in eastern Asia. In a similar fashion the second PC is compatible with fanning out of people from Southeast Asia and China, although it could also result from a major movement originating in the northernmost reaches of Asia.

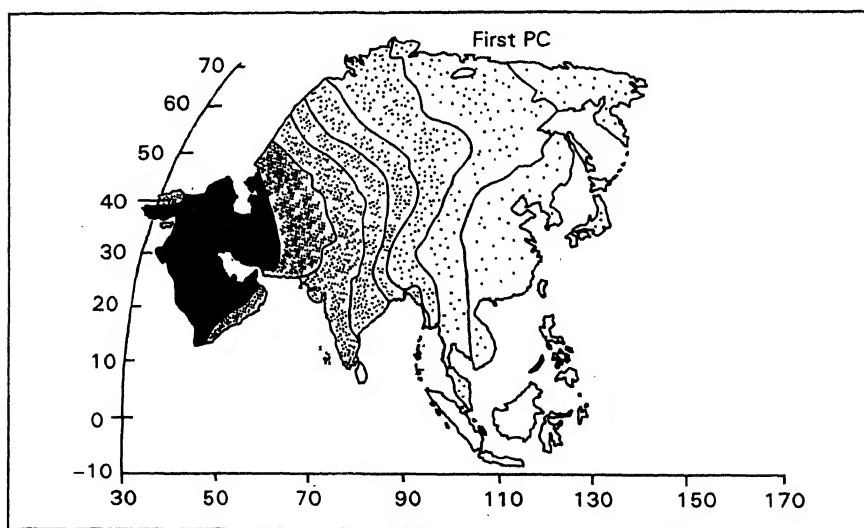


Fig. 6 Synthetic genetic map of the first principal component for Asia based on 69 genes for 42 populations [Cavalli-Sforza et al., 1994]

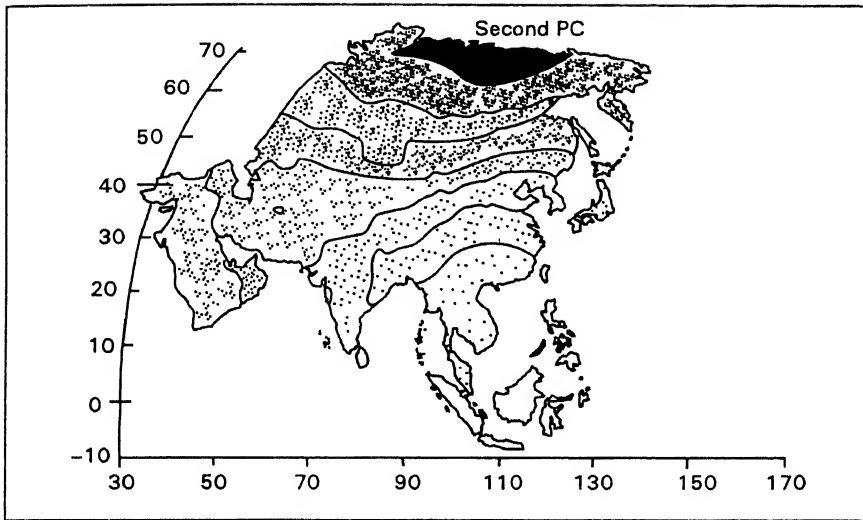


Fig. 7 Synthetic genetic map of the second principal component for Asia based on 69 genes for 42 populations [Cavalli-Sforza *et al.*, 1994]

In both these cases, the first explanation, namely fanning out of people from the Middle East and from China and Southeast Asia is far more likely. These are known to have been two independent centres of origin of cultivated plants, the Middle East being the earliest in the world around 10 kybp, and China and Southeast Asia a little later around 8 kybp. Cultivation permits substantial increases in population density. This numerical superiority as well as availability of stored grain and meat on hoof as a buffer permits agricultural people to expand into regions that were until then under hunting-gathering economy, replacing and absorbing the local populations and leaving definite genetic footprints. Excellent archaeological evidence from Europe provides conclusive evidence of such a process of a northward fanning out of farming people. It is then very likely that Asian populations today represent two major radiations of people out of two centres of origin of cultivation, one in the Middle East, and the other in China and Southeast Asia. The Indian population too must have been profoundly influenced by these two migrations, one through its northwestern frontiers near Khyber Pass in present-day Pakistan, and the other through the northeast near the China–Myanmar–India border in Manipur. The first one appears to be more significant, since it explains twice as much of the total variation.

Language families reveal people's ancestries and movements

Humans transmit not only genes but also cultural traits from one generation to the next. Some of these are extremely conservative, being transmitted quite faithfully from parents to offspring. Foremost amongst these is language; children almost invariably acquire their mother tongue from their parents and other relatives. Language and other

conservative traits such as practices relating to disposal of the dead are therefore excellent devices to trace historical changes. If this be so, linguistic and genetic divergence ought to go hand in hand. To test this proposition, Cavalli-Sforza et al. (1994) plotted genetic distance amongst members of a human group against the number of different languages spoken by members of the group (Fig. 8). The excellent correlation confirms our faith in languages as good markers for unravelling the ancestries and movements of people.

The languages of the world have been classified into a number of major families. There are of course a few which are stand-alones, which cannot be assigned to any family. Nahali, a tribal language of Central India and Burushaski, spoken by a small group of people on the border of Pakistan and Afghanistan are two such. But all other languages of India can be assigned to one of four major language families—Austic, Dravidian, Indo-European and Sino-Tibetan. An excellent information base on the speakers of these languages is provided by the People of India Project of the Anthropological Survey of India. This project involved assigning the entire Indian population to 4635 ethnic communities, and putting together detailed information on each of them through interviews with over 25,000 individual informants spread over all districts of India, along with compiling information from a variety of published sources [Joshi et al., 1993]. This project records as the mother tongue the number of languages of different families spoken by Indian ethnic communities as indicated in Table 1.

Table 1

Language family	No. of languages in India	No. of Indian ethnic communities	Global distribution
Austic	24	65	Southeast Asia, Eastern and Central India
Dravidian	35	1281	South and Central India, Pakistan, Iran
Indo-European	110	3094	Europe, West Asia, North, West & East India
Sino-Tibetan	130	207	China, Southeast Asia, India bordering Himalayas

It is reasonable to assume that speakers of these four language families represent at least four major lineages [Parpola, 1974]. The first question to ask is whether these language families developed within the country, or came in with migrations of people from outside the subcontinent. The geographical range of distribution of Austic, Indo-European and Sino-Tibetan speakers is extensive; India harbours only a minority of the languages within these families. The geographical range of distribution of Dravidian languages is however restricted largely to India; there are only two outlying populations—Brahui in Baluchistan and Elamite in Iran. Dravidian languages might then have developed within India. Others are less likely to have done so, for we have no evidence of any major technological innovations that could have served to carry speakers of those languages outside India.

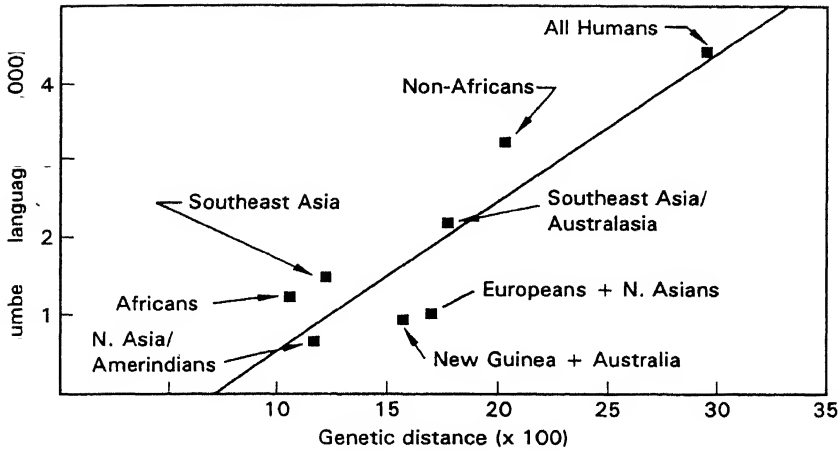


Fig. 8 Number of languages versus genetic distance in major regions of the world and for all of human populations [Cavalli-Sforza et al., 1994]

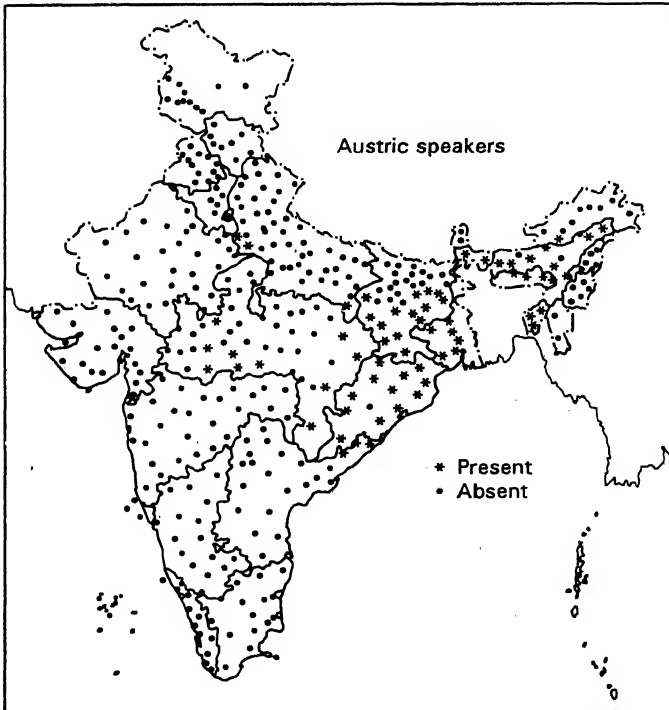


Fig. 9 District level distribution of Austric language speakers in India

Language and economy

We may look for evidence on how long the lineages belonging to different language families have been in India in two different ways. Firstly we may examine the current levels of economic activities of the communities speaking those languages and compare them with levels of economic activities of speakers of other language families. The tribal communities of India continue to extensively hunt and gather as well as practise low-input shifting cultivation. These communities are likely to have migrated to India relatively early, perhaps prior to the beginning of agriculture and animal husbandry. Some tribal groups or other speak languages belonging to each of the four families. Korkus, Mundas, Santals and Khasis speak Austric languages; Gonds and Oraons, Dravidian languages; Nagas and Kukis, Sino-Tibetan languages and Bhils and Varlis speak Indo-European languages (Figs. 9–12). But it is amongst Austric speakers that all communities are exclusively tribal. Outside India too, most Austric speaking communities practise very primitive technologies. This suggests that Austric speaking people may be the oldest inhabitants of India. They may be amongst the first group of *Homo sapiens* to have reached India, perhaps some 50–65 kybp. Since over 98% of Austric speakers today lie in Southeast Asia, they may have entered India from the northeast.

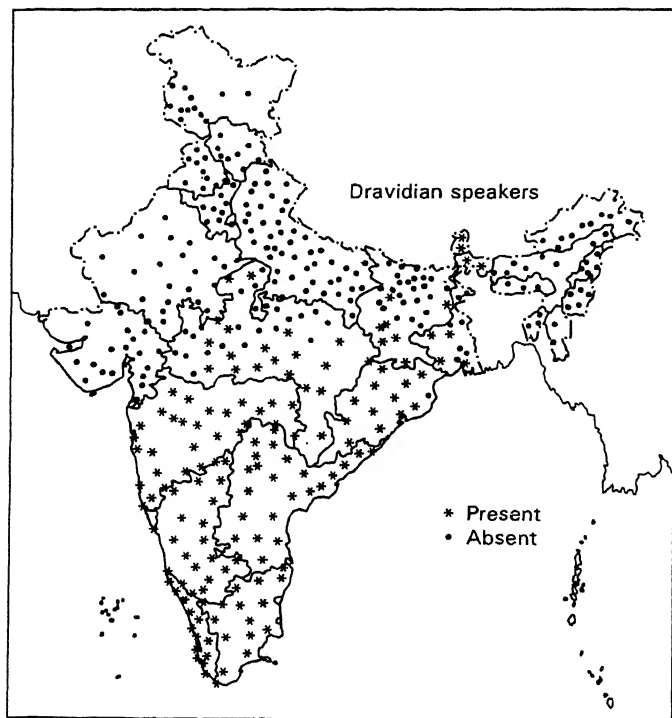


Fig. 10 District level distribution of Dravidian language speakers in India

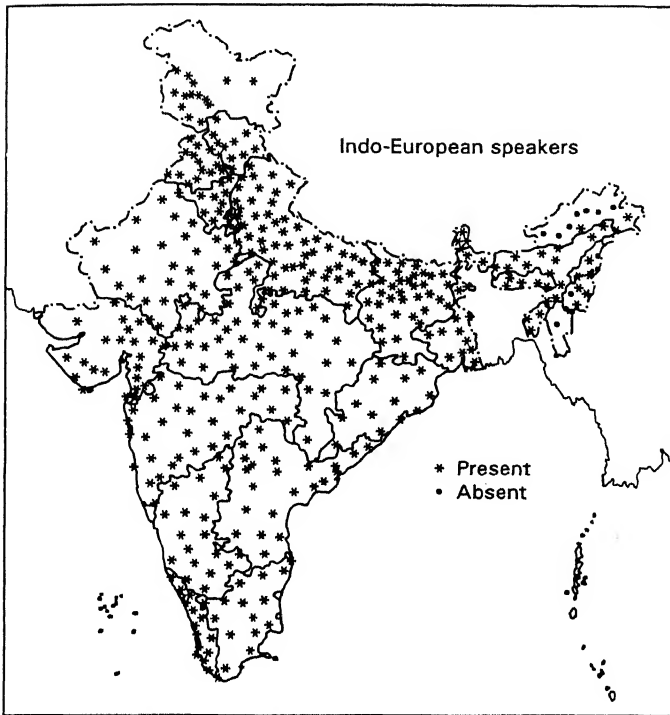


Fig. 11 District level distribution of Indo-European language speakers in India

Sino-Tibetan speakers of India also include many tribal groups, though they also include communities like the Maities of the Manipur valley practising advanced agriculture. Their concentration is along the Himalayas; only one community of West Bengal has reached mainland India. Many of them report having moved into India from Myanmar or China within the last few generations. They are therefore peripheral to the broader peopling of India.

The bulk of Indian mainland populations are Dravidian and Indo-European speakers. Both include communities at all economic levels from tribals to the most advanced cultivators, traders or pastoral groups. Many of the technologically less advanced amongst these communities such as the Dravidian speaking Kanians of Kerala or the Indo-European speaking Bhils of Rajasthan may have acquired these languages in more recent times through the influence of the economically more advanced mainstream societies. It is however notable that while there are several Dravidian speaking forest-dwelling tribal communities such as Gonds or Oraons in a matrix of more advanced Indo-European speaking communities, there are no enclaves of forest-dwelling tribal Indo-European speakers surrounded by more advanced Dravidian speaking communities. The tribal Indo-European speakers of South India are all nomadic communities such as Banjaras or Pardhis, with known history of migration from Rajasthan to South India in recent

centuries. This is strongly suggestive of Dravidians being older inhabitants of the Indian subcontinent, having been pushed southwards, surrounded by or converted to Indo-European languages by later arriving Indo-European speakers [Lal, 1974; Rakshit and Hirendra, 1980].

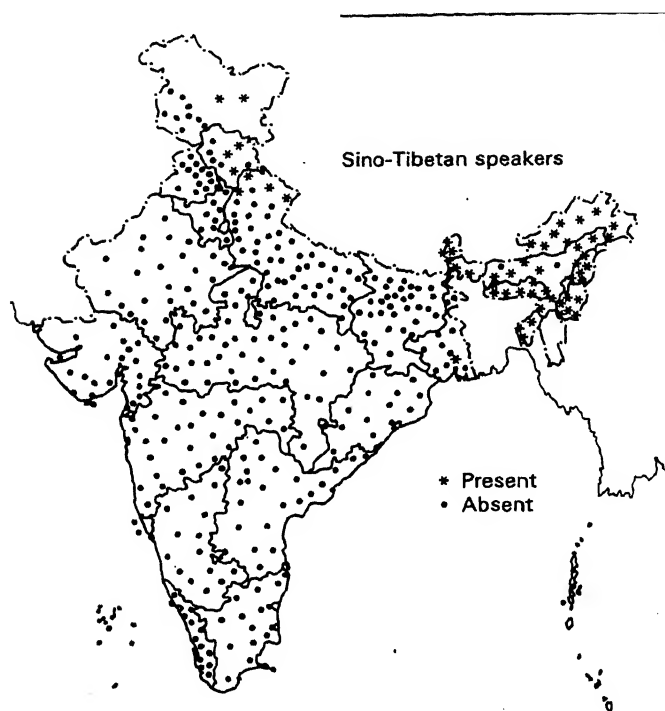


Fig. 12 District level distribution of Sino-Tibetan language speakers in India

One may then suggest the following sequence of migrations of these major language speaking groups into India: Austric–Dravidian–Indo-European. If this be correct, another interesting prediction follows. Austric languages having arrived in India earliest may show the most diversified vocabulary, Indo-European languages the least. To test this we have compiled words for universally used nouns such as mother, water, tree, etc. in several Austric, Dravidian, Indo-European and Sino-Tibetan languages. While a more objective analysis of the extent of such variation is under way, it appears that Austric languages show the greatest and Indo-European the least divergence.

Archaeological evidence

While tool-using *Homo erectus* populations have been in India for over 500 kyears BP, fossil human remains appear only after 45–50 kybp, associated with Middle Palaeolithic or Stone Age tools [Agarwal, 1982; Agarwal and Ghosh, 1973; Agarwal and

Kusumgar, 1974; Kennedy, 1980] (Fig. 13). It has been suggested that these sites fall in two groups, the northern sites showing affinities with the Mousterian tool industries of Europe, while the southern sites show cultural antecedents in Lower Palaeolithic. This may reflect two separate streams of migration of newly expanding *Homo sapiens* populations, one coming into India from the northwest, the second from the northeast. One may surmise that the stream coming in from the northeast may have included early speakers of Austric languages.

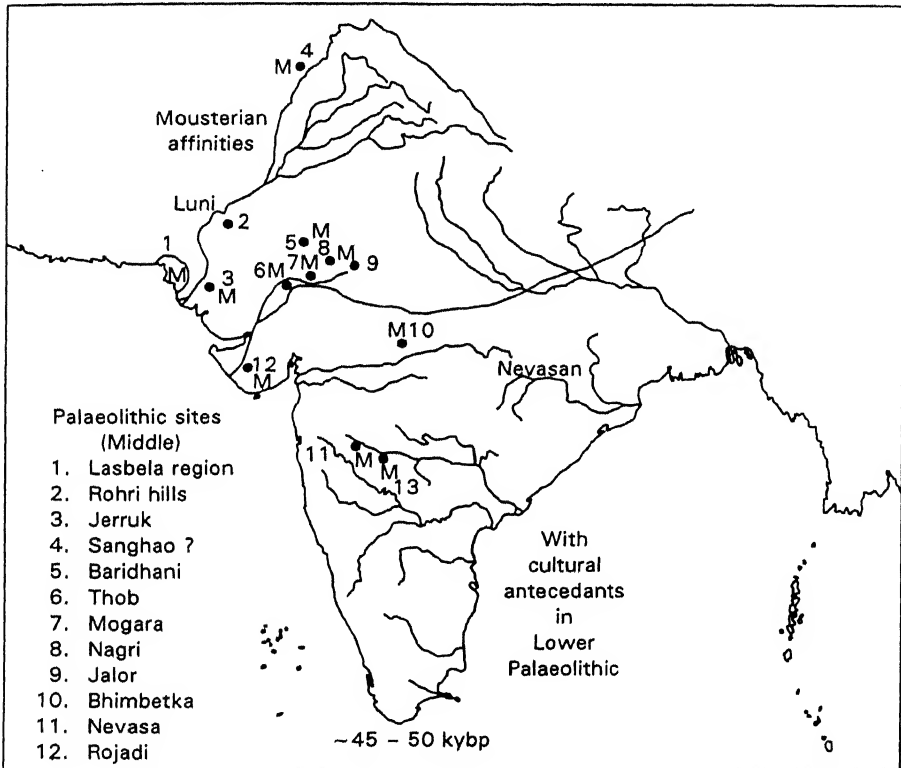


Fig. 13 Major Middle Palaeolithic sites of India

The next important event on the Indian archaeological scene is the beginning of cultivation of crops and use of pottery [Agarwal and Pande, 1977; Megaw, 1977; Vishnu-Mittre, 1977; Jarrige and Lechevallier, 1973; Dani et al., 1967; Vishnu-Mittre, 1989] (Figs. 14 and 15). Cultivation of plants evidently reached India around 6 kybp simultaneously from two different directions, from the two centres of origin in the Middle East, and China and Southeast Asia. The steady advance beyond this stage seems however to have been primarily driven by the crop-animal complex derived from the mideast, reaching the tip of southern India some 4000 years later around 2 k years BP. The diffusion of pottery traditions, which arise in response to the need to store and cook grain, shows

similar evidence of the two influences from northwest and northeast, with the western influence predominating over much of the country. Thus the Black and Red Ware reflect western, while the Cordedware reflects Chinese influence [Sankalia, 1974; Allchin and Allchin, 1988; Goudie, 1977; Brice, 1977; Rao, 1965, 1969].

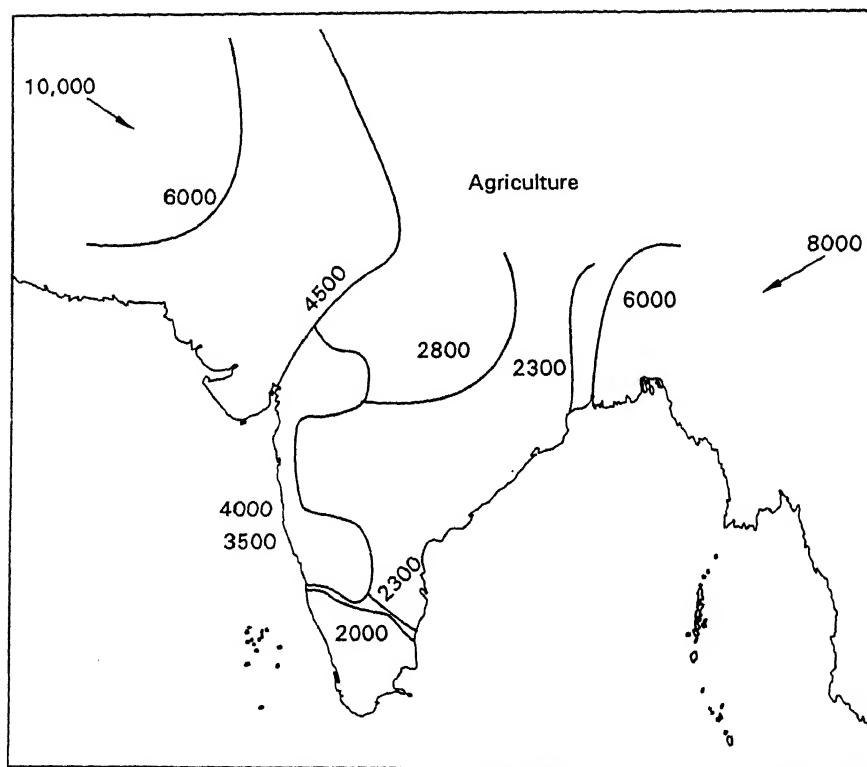


Fig. 14 *Contours of earliest dates of definite evidence of cultivation of crops in India*

It is likely that the farmers entering India from the northwestern passage were either Dravidian or Indo-European speakers; those entering the subcontinent from the northeastern passage may have been Sino-Tibetan or Austric speakers. If, as the linguistic evidence suggests, Dravidian speakers entered India well before Indo-European speakers then Mideastern farmers entering India from the northwest may have been Dravidian speakers. The remnants of related languages, Elamite and Brahui in Iran and Pakistan, are consistent with such a migration of Dravidian speakers from the Middle East to India.

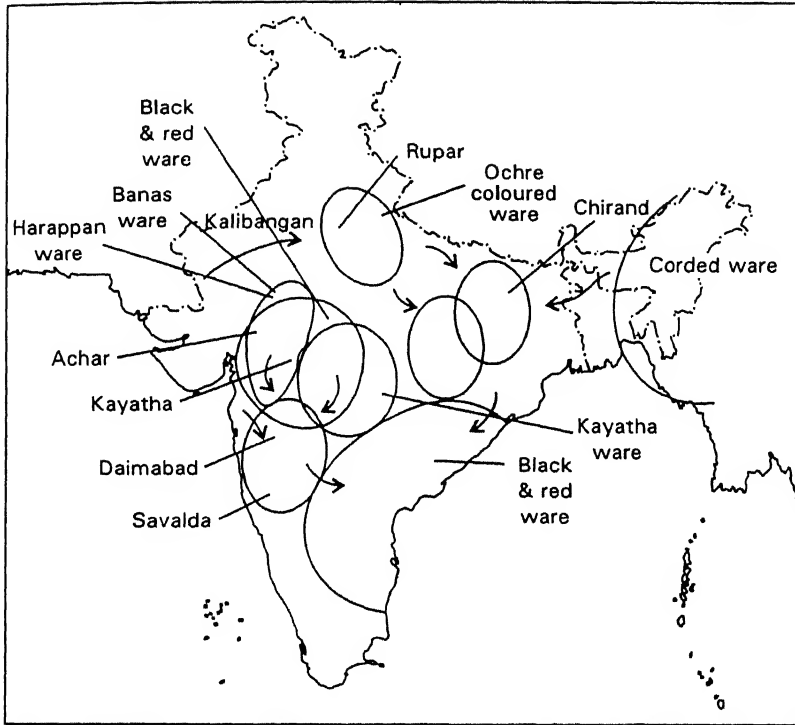


Fig. 15 *Major pottery traditions of India*

Horse and iron as pointers of heritage

If this is true, then the Indo-European speakers must have come to India with some other major advantage. Two technological innovations, known to have originated outside of India, are excellent candidates. They are the domestication of the horse, around 6 kybp on the shores of the Black Sea in present Ukraine, and the use of iron, around 5 kybp in Anatolia in present-day Turkey. Riding of horses or hitching them to carts greatly increases the mobility and the military or trading capabilities of a group. While cattle, sheep, goat and pigs were all domesticated in the Middle East around 10 kybp, the horse was domesticated 4000 years later in a separate centre in the Asian steppes. The most favoured theory of the spread of Indo-European languages today is that it was the language of these horse people who came to dominate Europe, West Asia and much of India over the next 4000 years. As a ruling class, they are believed to have imposed their language over Europe, without making any major genetic contributions to the populations. They may have wielded parallel influence in India.

The horse appears in archaeological records between 2000 to 500 years after the first appearance of cultivation of crops and husbanding of cattle, sheep, goat and pigs in different parts of India (Fig. 16). Particular styles of burial appear to accompany the horse people. These burial styles show links with styles noted in the Central Asian homeland of Indo-European speakers, strengthening our belief in the possibility that the Indo-European speakers indeed made their way to India propelled by the advantage that the control over horses conferred.

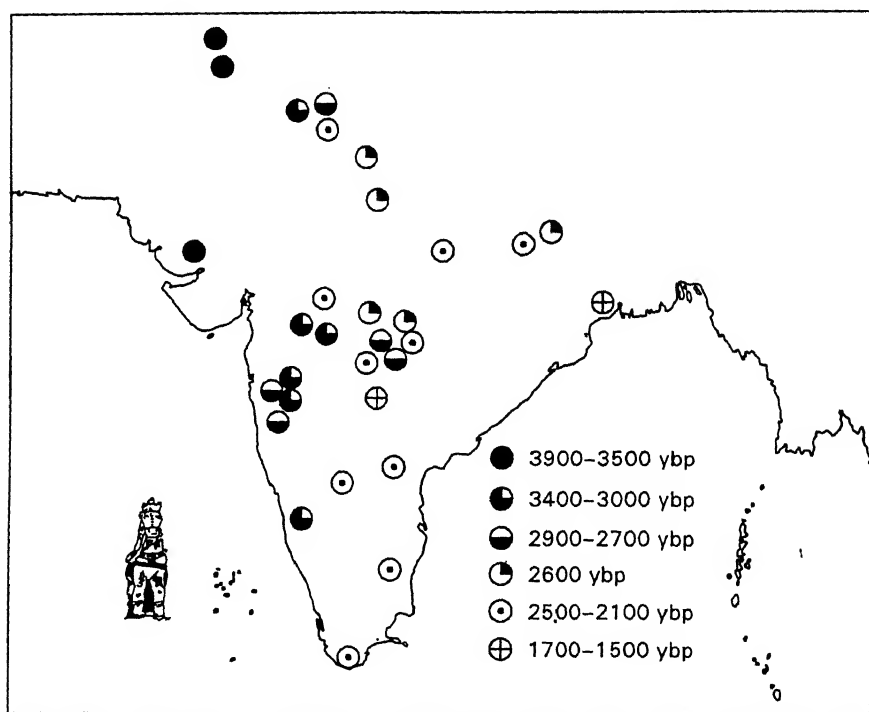


Fig. 16 *First dates of appearance of domesticated horse in different parts of India*

The people associated with Vedic traditions and Sanskrit definitely used horses, and may have been one group, though perhaps not the only group of Indo-European speakers to enter the subcontinent. These people also seem to have been associated with cremation as a method of disposal of the dead. Cremation is today the dominant mode amongst most Indo-European speaking communities of India while burial is common amongst Dravidian speaking communities, especially those affected little by the process of Sanskritisation (Fig. 17). This also suggests that Indo-European speakers came to India after Dravidian speakers, probably associated with the use of horses and the practice of cremation.

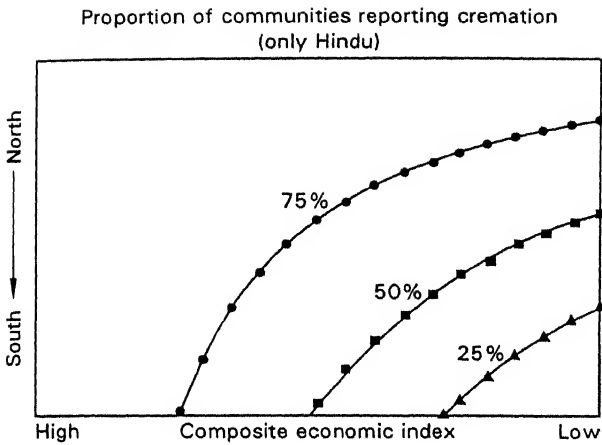


Fig. 17 The distribution of cremation vs burial of the dead in mainland India along a north-south geographical axis and amongst different social strata

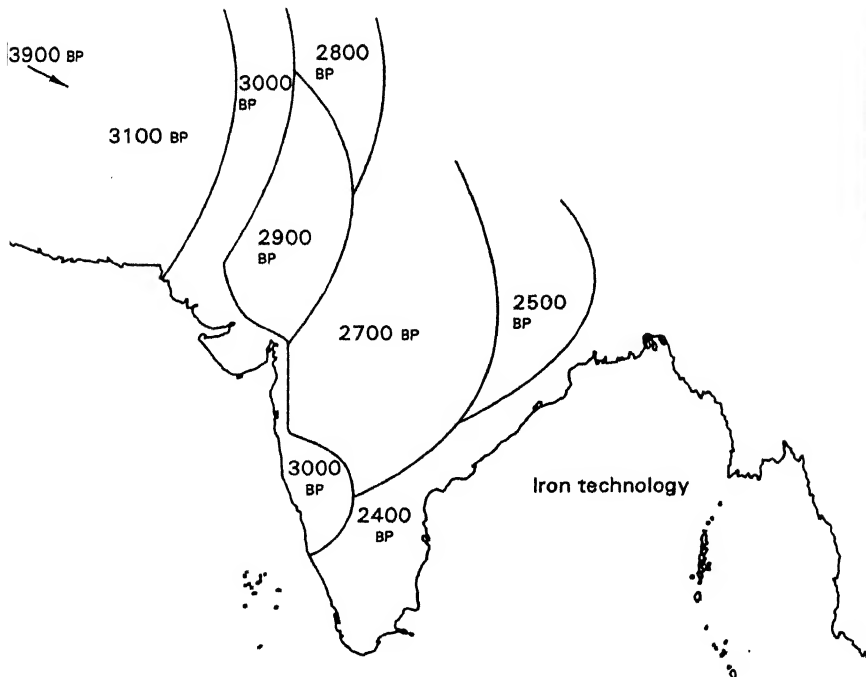


Fig. 18 The earliest known dates of appearance of iron technology in different parts of India

It is also possible that it was the use of iron that conferred an important advantage to certain groups of people migrating to India—groups that may have included speakers of Indo-European languages. The archaeological evidence suggests that use of iron is not necessarily associated with that of the horse, and appears either later than or ahead of the former in different parts of the country (Figs. 18 and 19). It is then likely that iron was brought to India by people other than the horse people, i.e., people other than Vedic people. Indeed, there may have been many waves of Indo-European speakers into India that may have brought into the country different languages of that family. Thus, some linguists believe that the present-day Indo-European languages came to India in at least two distinct streams, the first stream bringing in languages related to Bengali, Oriya, Marathi, Sindhi and Kashmiri, and the second stream of languages related to Punjabi, Hindi and Rajasthani [Gupta, 1979; Misra and Bagor, 1973; Goude, Allchin and Hegde; Agarwal, 1971; Chakrabathi, 1976; Banerjee, 1965; Stein, 1984; Jha, 1981; Parasher, 1992; Emmerick; Verma, 1971].

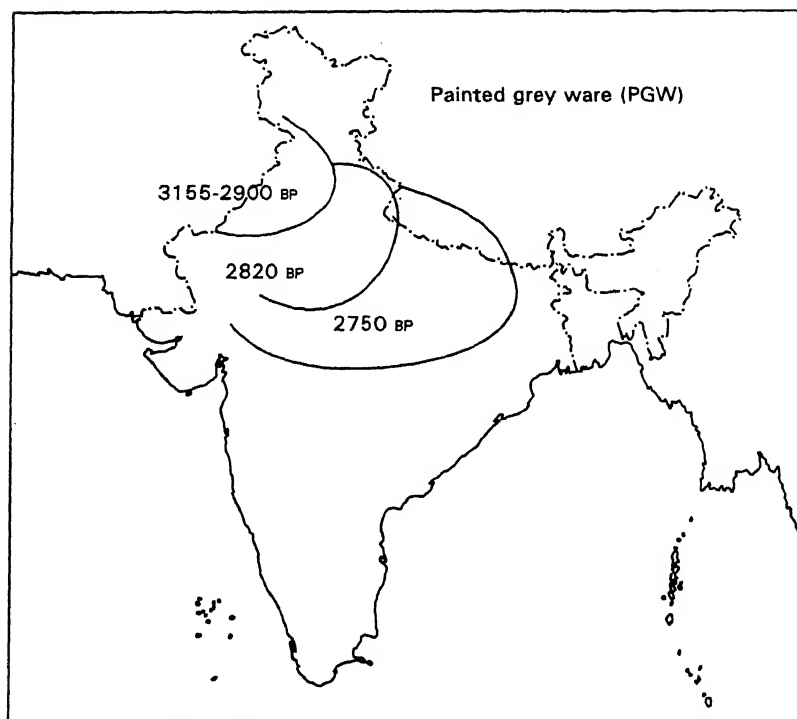


Fig. 19 Known dates of appearance of painted grey ware pottery known to be associated with users of iron technology

It is not at all clear whether the Harappan people spoke Dravidian or Indo-European languages. This civilisation is contemporaneous with the first appearance of the horse, most likely associated with Indo-European speakers in the archaeological record. It

could therefore have been an Indo-European speaking civilisation. But there is a greater possibility that it may have emerged out of the earlier Dravidian speaking communities of agriculturists. What seems more plausible is the equation of *Dasas* of Vedic people with the earliest, probably Austric speaking hunter-gatherers, and *Dasyus* with the Dravidian speaking cultivating communities. It is notable that the Vedic people were engaged in a violent conflict with *Dasyus*; such conflict may relate to struggle over fertile land [Possehl, 1979].

A plausible scenario

There are then many still unanswered questions pertaining to how our subcontinent was peopled. But the most plausible scenario is the one depicted in Figs. 20–23. The earliest of the modern *Homo sapiens* migrating into India, perhaps 50,000 years ago may have been speakers of Austric languages with the advantage conferred by the mastery over a symbolic language. Their genetic footprints may be discerned in the trends evident in

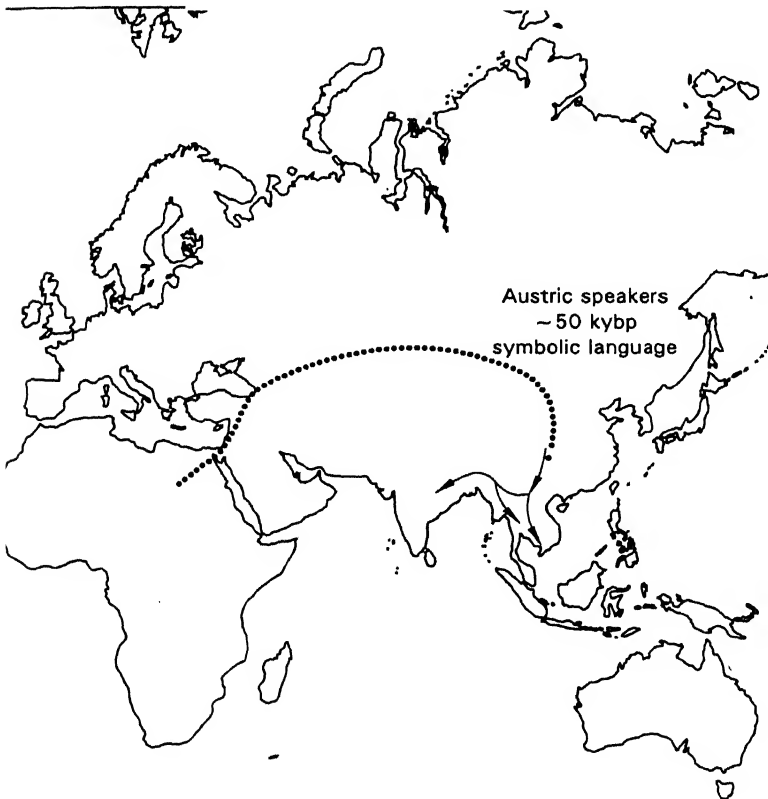


Fig. 20 A possible scenario of the earliest migrations of Austric speaking people into India

the second PC of the synthetic genetic map of Asia. The next major waves of migrations around 6 kypb may have been those of wheat cultivators from the Middle East and the rice cultivators from China and Southeast Asia. The former are likely to have been Dravidian speakers and probably contributed to the trend evident in the first PC of the synthetic genetic map of Asia [Allchin, 1963; Badam, 1984]; the latter may have been Sino-Tibetan speakers who would have contributed further to the trend revealed by the second PC. The latest major migration, around 4 kypb, may have included several waves of Indo-European speakers equipped with horses and iron technology.

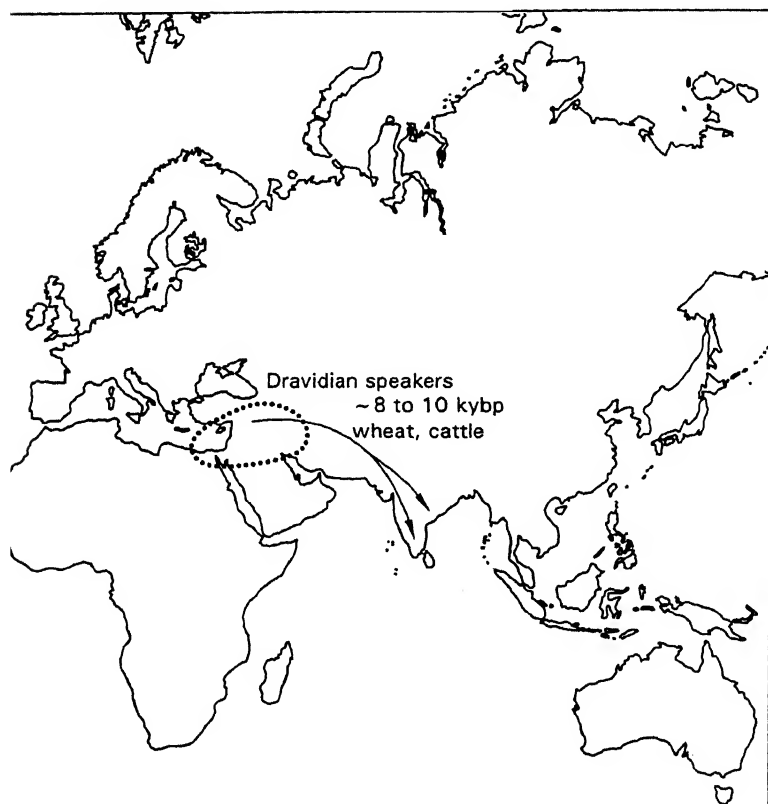


Fig. 21 *A possible scenario of migrations of Dravidian speaking people into India*

These might have been the most massive migrations peopling India. Others have followed, largely from the west, through the Khyber Pass on the northwestern frontier of the subcontinent. These seem to have been propelled by superior weaponry, increasingly better control over horses and, finally, sea-going ships. Such significant innovations may include some of the following. An important early development in weaponry was the composite angular bow which appeared in West Asia around 5 kypb. Bending through the length of the limb, releasing this bow string produced

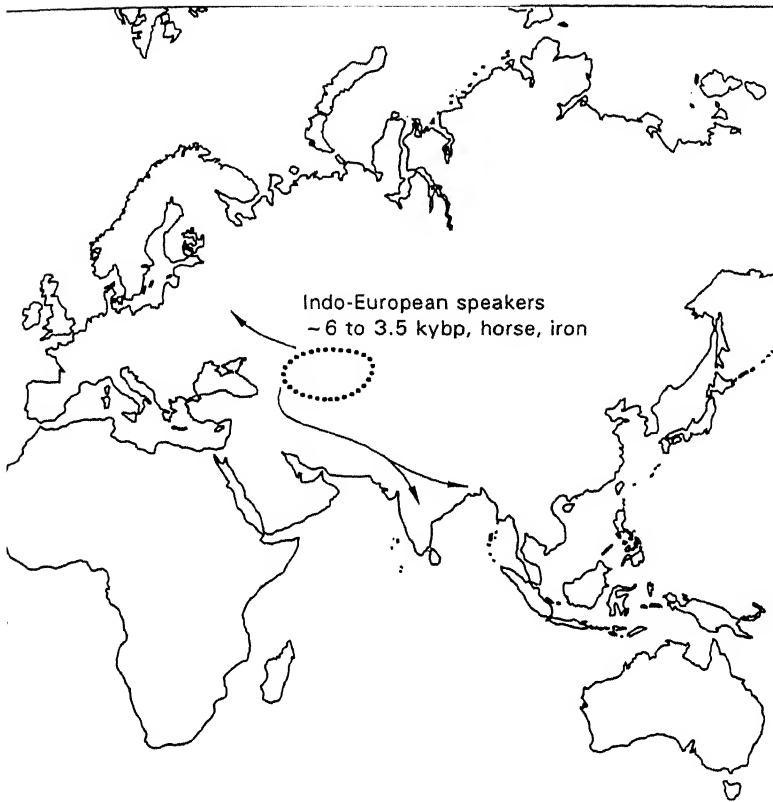


Fig. 22 A possible scenario of migrations of Indo-European speaking people into India

no kick, leading to a smooth and accurate shot. The extremely long draw length of over one metre led to a greatly enhanced cast. A crucial piece of equipment associated with control over the horse is the stirrup, which helps in balancing the rider and permits him to stand up and throw the lance. The earliest form of the stirrup was a string with two loops on either side for the rider's foot. The first known instance of iron stirrups comes from China in sixth century AD, reaching Iran by the 7th century and arriving in India with Turkish warriors in the 11th century. Another significant invention was the iron horseshoe, first known from Siberia in the 9th century AD, reaching India with Turkish warriors in the 13th century AD. Gunpowder was invented in China around AD 100 and slowly reached Iran, Arabia and finally Europe with the Mongols around AD 1400. It reached India with the arrival of the first Mughal emperor Babur, who used it in the First Battle of Panipat in AD 1526 (Fig. 24). The early cannons in India were made by welding together many iron rods. The Europeans introduced cast iron cannons in the next century which could fire more accurate and powerful volleys. The Europeans also developed superior ocean-going vessels from which cannons could be fired, by the 16th century [Deloche, 1983; Habib, 1992].

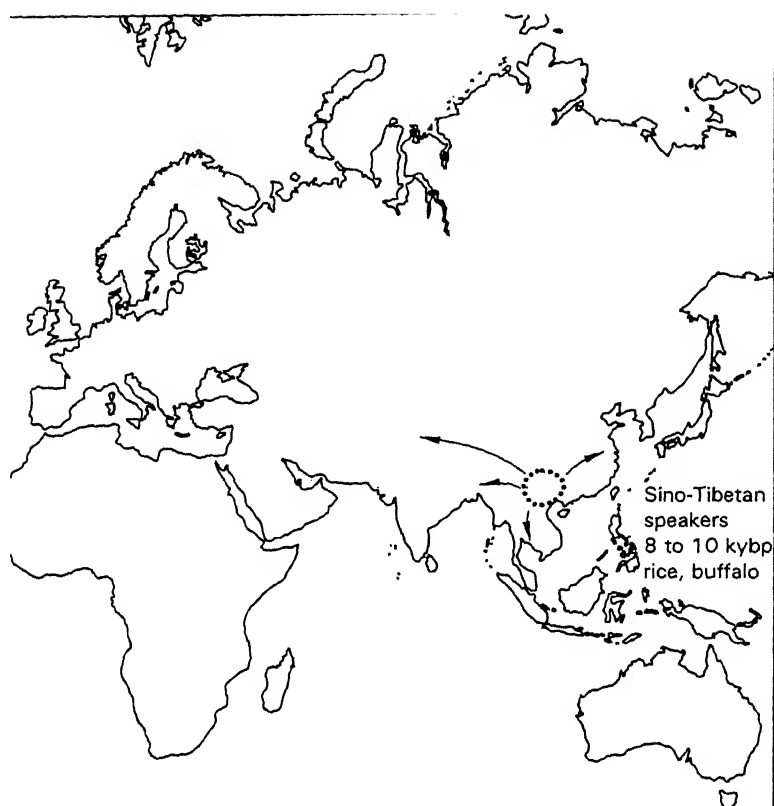


Fig. 23 A possible scenario of migrations of Sino-Tibetan speaking people into India

These many developments taking place in China, Central Asia and finally Europe brought in many people enjoying a military advantage (Fig. 25). The number of people thus coming in were probably not very large, but they contributed immensely to the cultural diversity of the country by bringing in new languages, new religions, and of course new technologies. Among these technologies was the spinning wheel, apparently invented in China and brought to Europe by the Mongols around the 12th century AD. It seems to have reached India in the 13th–14th century and created a tremendous commercial potential for textile production in India. Similarly, Indian agriculture too must have been greatly influenced by the introduction of the Persian wheel, first referred to by Babur in 1526–30 in his memoir, *Babur Nama*.

With these many streams of *Homo sapiens* coming into the country over 50,000 years or more, India has developed what Cavalli-Sforza calls an incredibly complex genetic landscape. Our mtDNA data on 101 Indians permits us to estimate the time to common ancestry of our people on the basis of the pairwise differences in the mtDNA sequences. These estimates of course depend on the assumed value of mutation rates; but

65,000 years is a reasonable estimate for the modal value of 9 pairwise differences (Fig. 26). So the Indian population has been put together by people drawn from many different streams ultimately derived from the major expansion of non-African *Homo sapiens* around this time.

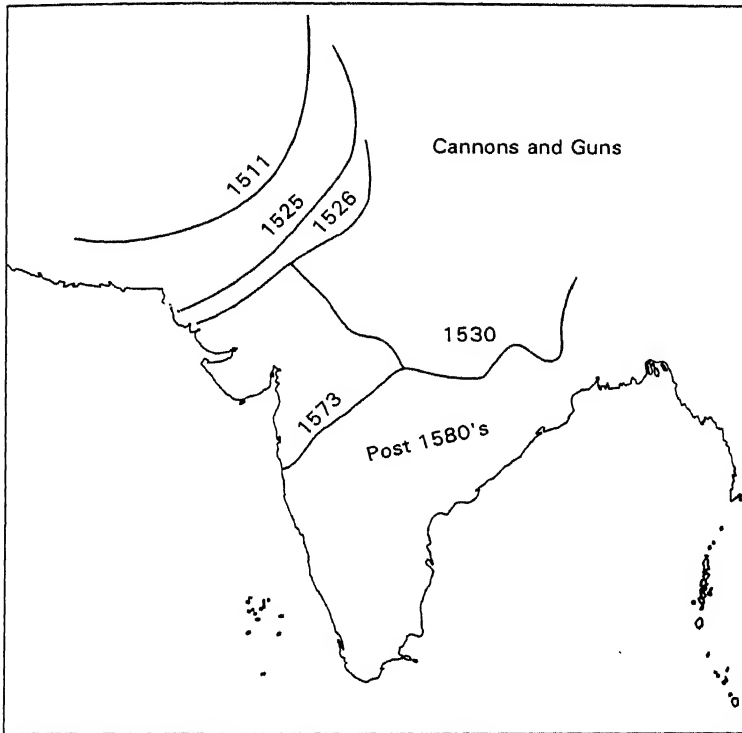


Fig. 24 The earliest known usage of cannons and guns in India

A segmented society

What the Indian population is remarkable for is the segmentation of this large population into thousands of endogamous groups. The data of the People of India Project recognises 4635 such ethnic communities. Many of these are however clusters of endogamous groups with similar traditional occupations and social status. The actual number of endogamous groups is decidedly much larger, of the order of 50,000 to 60,000 [Joshi, Gadgil and Patil, 1993; Gadgil and Malhotra, 1983]. This persistence of tribe-like endogamous groups, characteristic of hunting-gathering-shifting cultivation stage all over the world, in a complex agrarian and now industrial society of India, is a unique phenomenon. It seems to be the result of a peculiarly Indian tradition of subjugation and isolation, rather than the worldwide practice of elimination or assimilation of subordinated communities by the dominant groups.

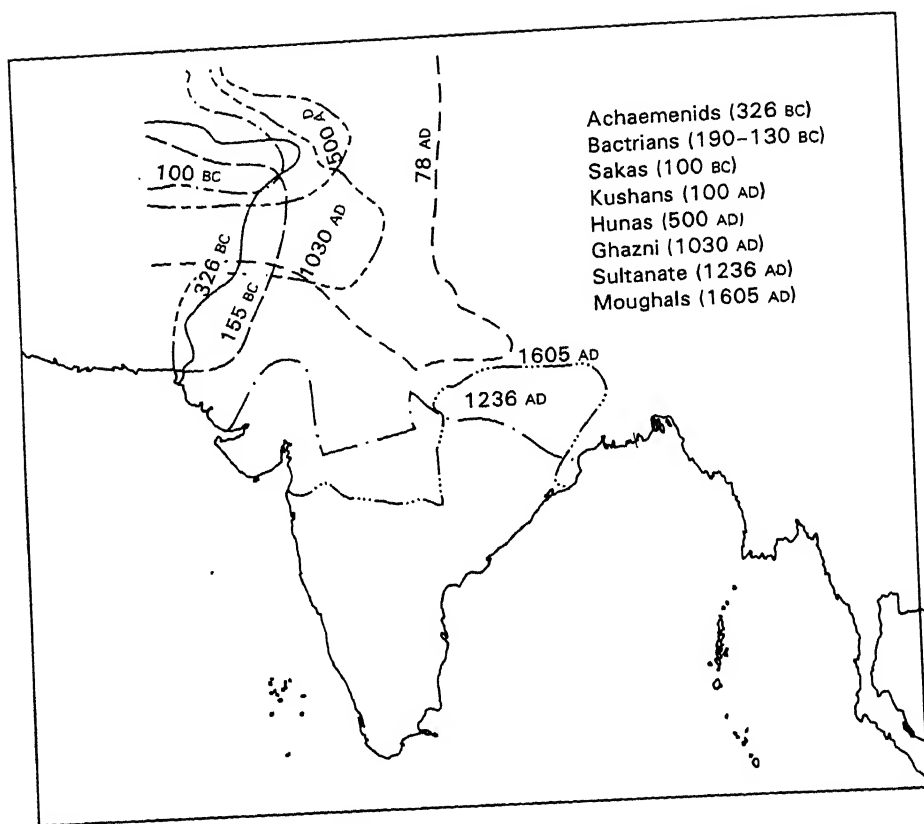


Fig. 25 Migrations of people enjoying a military advantage through the northwestern passage into India between 300 BC and 1600 AD.

Our mtDNA studies provide some notable insights into the structure of this social mosaic. For this purpose we chose two communities, Haviks and Mukris from the same district of Uttara Kannada. Haviks are a Brahmin group well known for their skills at growing multi-storeyed spice gardens of cardamom, pepper and betelnut. They also perform priestly functions, and are today prominent in many white-collar occupations. Their current population is around 100,000 individuals concentrated in an area of about 20,000 sq km. The Mukris, on the contrary, are members of a scheduled caste, earlier treated as untouchables. Their current population numbers around 9000 individuals concentrated in an area of 2000 sq km. They continue to indulge in substantial amounts of hunting, gathering and fishing to date, and serve as unskilled labour on Havik and other farms.

Figure 26 depicts the neighbour joining phylogenetic tree for 48 Haviks, 43 Mukris, 7 Kadars and a few other Indians. Note that Haviks and Mukris, although they lie at opposite ends of the social hierarchy, do not constitute two distinct trunks! Their sequences are intermingled, suggesting past genetic exchanges, although these may

have occurred well before the formation of the Indian caste system some 2000 years ago; indeed they may even derive from the time of common ancestry some 65,000 years ago, perhaps as a part of population expansion of non-Africans outside India.

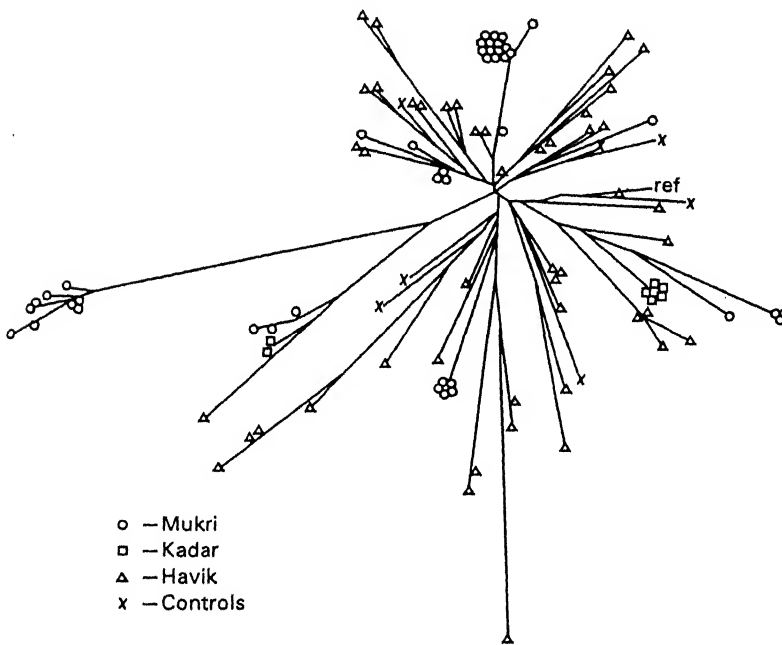


Fig. 26 Neighbour joining tree depicting 101 Indian sequences [Mountain et al., 1995]

But intermingled as they are, the Havik sequences form a distinctive star-like pattern with many short branches joining the centre, unlike the Mukri sequences which are bunched in a few clusters on long branches. The star-like Havik pattern is suggestive of a history of population expansion, while the clustered Mukri pattern suggests a long history of a stationary population, or a population that has experienced several bottle-necks. This is further brought out in the distribution of pairwise mtDNA base pair sequence differences for the Havik and Mukri populations (Fig. 27). The unimodal pattern for Haviks is compatible with a history of population growth while the multimodal Mukri pattern indicates a history of population stationarity or bottle-necks.

Such differences in genetic structure suggestive of different population histories have been suggested from other human populations earlier, but never before for two population groups living together in such a restricted geographical locality as a single district of Uttara Kannada. This reflects the unique history of Indian population, with dominant groups like Haviks enjoying high levels of resource access and expanding in numbers and range, while subjugated populations like Mukris existed side by side with much more limited resource access and stagnant populations (Fig. 28).

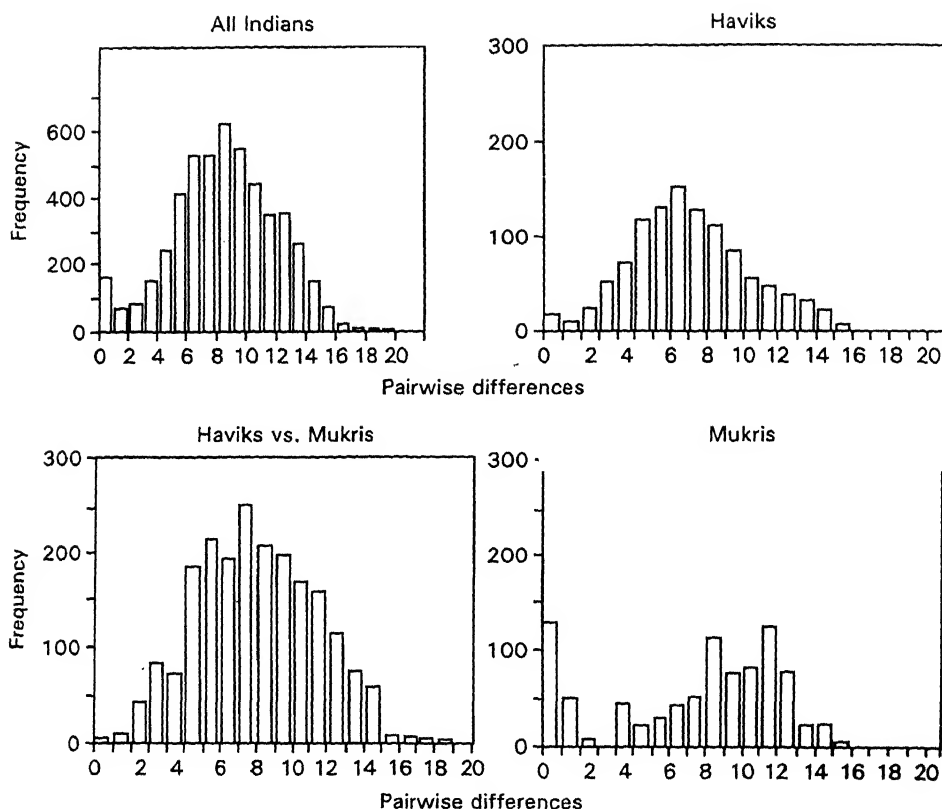


Fig. 27 *Distribution of pairwise differences in mitochondrial DNA sequences of 101 Indians [Mountain et al., 1995]*

Such scenarios have probably characterised the Indian social mosaic for long, perhaps since the beginning of cultivation and animal husbandry 6000 years ago. As groups with technologies conferring superiority in resource appropriation have migrated into and spread throughout India, they have subjugated other groups, restricted their resource access and permitted their continued existence, while the dominant groups have themselves grown in number and expanded in geographical range, perhaps dividing further into more endogamous groups.

This process of maintenance of a large number of communities in isolation from each other has been accompanied by extreme specialisation of occupation. It is perhaps this specialisation of occupation that has prevented Indians from cross-fertilisation of ideas and innovations, so that the Indian society has always been at the receiving end of technological innovations.

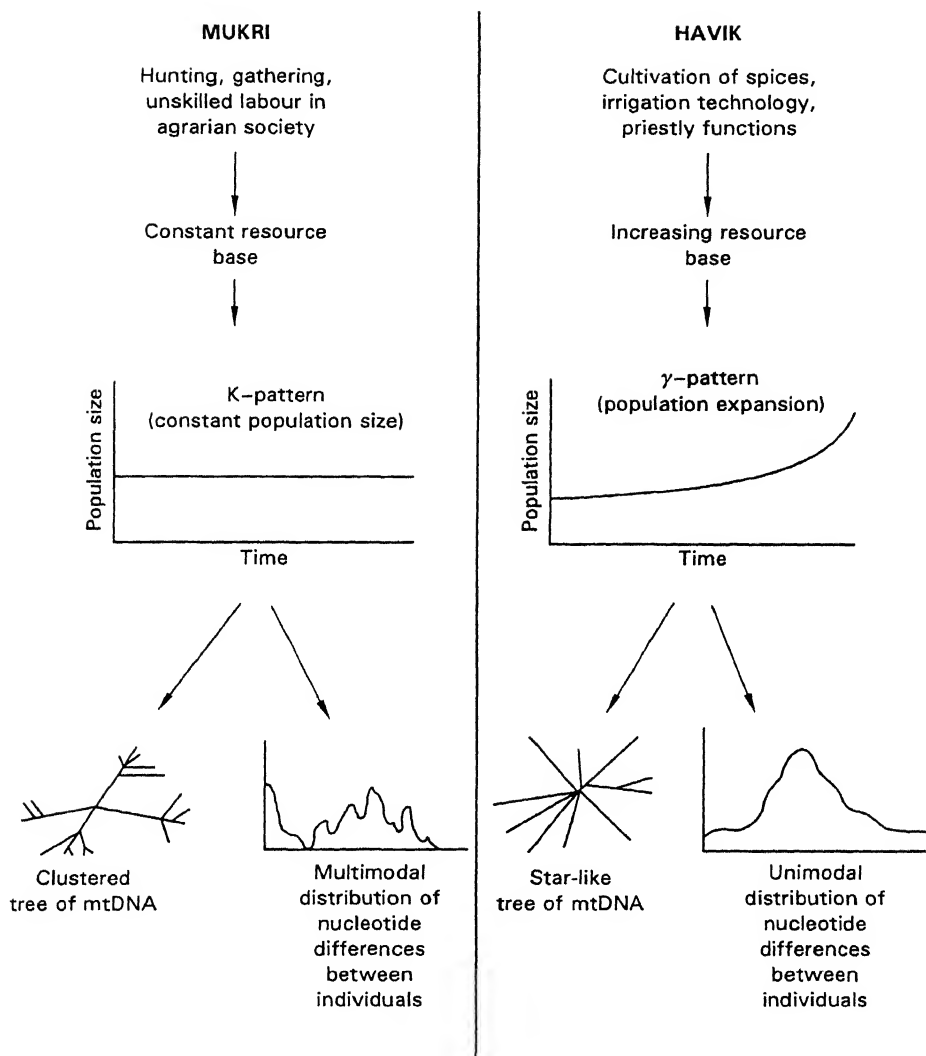


Fig. 28 Possible scenarios leading to the difference between the trees and pairwise difference distributions of the Mukri and Havik samples

Acknowledgements

We are grateful to our co-investigators in the population genetic study, Joanna L. Mountain, Joan M. Herbert, Peter A. Underhill, Chris Ottolenghi, L.L. Cavalli-Sforza and Silanjan Bhattacharya. We were greatly helped in the field work involved by Anindya

Sinha, A. Maithili and Vijayakumari of the Dr. Baliga College of Arts and Science, Kumta. Prema Iyer provided valuable assistance in investigating subsistence strategies of Haviks and Mukris in the field. M.D. Subash Chandran, K.M. Hegde, Nagu Mukri, Masti Mukri and many other friends from Uttara Kannada have also greatly helped us understand this society and its history. We are grateful to Dr. K.S. Singh and his colleagues in the Anthropological Survey of India for making the People of India dataset available, and for many stimulating discussions. This work has been supported by grants from the Ministry of Environment and Forests, Government of India, and from the Anthropological Survey of India.

References

1. Agarwal, D.P. (1971). *The Copper Bronze Age in India*. Delhi.
2. Agarwal, D.P. (1982). *The Archaeology of India*. London and Malmo.
3. Agarwal, D.P. and Ghosh, A. (1973). *Radiocarbon and Indian Archaeology*. Bombay.
4. Agarwal, D.P. and Kusumgar, S. (1974). *Prehistoric Chronology and Radiocarbon dating in India*. New Delhi.
5. Agarwal, D.P. and Pande, B.M. (ed.) (1977). *Ecology and Archaeology of Western India*. Delhi.
6. Allchin, B. and Allchin, R. (1988). *The Rise of Civilization in India and Pakistan*. Cambridge World Archaeology. Cambridge University Press, Cambridge.
7. Allchin, F.R. (1963). *Neolithic Cattle-keepers of South India*. Cambridge.
8. Badam G.L. (1984). Holocene faunal material from India with special reference to domesticated animals. In Juliet Clutton-Brock and Caroline Grigson (eds.). *Animals and Archaeology: Early Herders and their Flocks*. Oxford. 339–353.
9. Ballinger S.W., Schurr, T.G., Torroni, A., Gan, Y.Y., Hodge, J.A., Hassan, K., Chen, K.H., et.al. (1992). Southeast Asian mitochondrial DNA analysis reveals genetic continuity of ancient mongoloid migrations. *Genetics*. **130**, 139–152.
10. Banerjee, N.R. (1965). *The Iron Age in India*. Delhi.
11. Brice, W.C. (ed.) (1977). *Environmental History of the Near and Middle East*. London.
12. Cavalli-Sforza, L.L., Menozzi, P. and Piazza, A. (1994). *The History and Geography of Human Genes*, pp. 541. Princeton University Press, Princeton, and *Genetic Maps*, 518.
13. Chakrabarti, D.K. (1976). The beginning of Iron in India. *Antiquity*. **50**, 114–24.
14. Dani, A.H. et al. (1967). Timargarh and the Gandhara grave culture. *Ancient Pakistan*. **3**, 407.
15. Deloche, J. (1983). Geographical considerations in the localisation of ancient sea-ports of India. *The Indian Economic and Social History Review*. **20**, (4) 439–448.
16. Emmerick, R.E. Indo-Iranian Languages. *Encyclopaedia Britannica*. **9**, 438–57.
17. Gadgil, M. and Guha, R. (1992). *This Fissured Land: An Ecological History of India*. Oxford University Press, New Delhi and University of California Press, Berkeley.
18. Gadgil, M. and Malhotra, K.C. (1983). Adaptive significance of the Indian caste system: an ecological perspective. *Annals of Human Biology*. **10**, 465–478.
19. Goude, A., Allchin, B. and Hegde, K.T.M. Former extensions of the Great Indian Sand Desert. *The Geographical Journal*. **139**, 243–57.
20. Goudie, A.S. (1977). *Environmental Change*. Oxford.
21. Gupta, S.P. (1979). *Archaeology of Soviet Central Asia and the Indian Borderlands*. Delhi. **1**.
22. Habib, I. (1992). Pursuing the history of Indian technology: Pre-modern modes of transmission of power. *Social Scientist*. **20**, (2&3), 22.

23. Jarrige, J.F. and Lechevallier, M. (1973). Excavations at Mehrgarh. In M. Taddei (ed.) *South Asian Archaeology*. 77, 463–535.
24. Jha, D.N. (1981). Relevance of Peasant state and Society to Pallava-Chola times. *The Indian Historical Review*. 8, (1&2), 74–94.
25. Joshi, N.V., Gadgil, M. and Patil, S. (1993). Exploring cultural diversity of the people of India. *Current Science*. 64, (1), 10–17.
26. Kennedy, K.A.R. (1980). Prehistoric skeletal records of man in South Asia. *Annual Review of Anthropology*. 9, 391–432.
27. Lal, P. (1974). The tribal man in India: A study in the ecology of the primitive communities. In M.S. Mani (ed.) *Ecology and Biogeography in India*. The Hague. 281–329.
28. Megaw, J.V.S. (1977). *Hunters, Gatherers and First Farmers Beyond Europe*. Leicester.
29. Misra, V.N. and Bagor (1973). Late Mesolithic settlement in northwest India. *World Archaeology*, 5, 92–110.
30. Mountain, J.L., Hebert, J.M., Bhattacharyya, S., Underhill, P.A., Ottolenghi, C., Gadgil, M. and Cavalli-Sforza, L.L. (1995). Demographic history of India and mtDNA-sequence diversity *Am. J. Hum. Genet.* 56, 979–992.
31. Parasher, A. (1992). Nature of society and civilization in early Deccan. *Indian Economic and Social History Review*. 29, (4), 437–477.
32. Parpola, A. (1974). On the protohistory of the Indian languages in the light of archaeological, linguistic and religious evidence: an attempt at integration. In Van Lohuizen (ed.) *South Asian Archaeology*, 73.
33. Possehl, G.L. (1979). *Ancient Cities of Indus*. New Delhi.
34. Rakshit, Hirendra K. (1980). Ethnohistory of the tribal population of middle India. *Journal of Indian Anthropological Society*. 15, 97–112.
35. Rao, N.M.S. (1965). *The Stone Age Hill Dwellers of Tekkalakota*. Ponna.
36. Rao, N.M.S. (1969). *Excavations at Sangankollu*. Ponna.
37. Sankalia, H.D. (1974). *Prehistory and Protohistory of India and Pakistan*. 2nd edn. Ponna.
38. Stein, Burton. (1984). Politics, Peasants and the deconstruction of feudalism in medieval India. *The Journal of Peasant Studies*. 12, (2&3), 54–86.
39. Verma, B.S. (1971). Excavations at Chirand. *Puratattava*. 4, 19–23.
40. Vigilant, L., Stoneking, M., Harpending, H., Hawkes, K. and Wilson, A.C. (1991). African populations and the evolution of human mitochondrial DNA. *Science*. 253, 1503–1507.
41. Vishnu-Mittre. (1977). India: local and introduced crops. In J. Hutchinson, G. Clark, E.M. Jope and R. Riley (eds.). *The Early History of Agriculture*. London.
42. Vishnu-Mittre. (1989). Forty years of Archaeobotanical research in South Asia. *Man and Environment*. XIV, (1), 1–16.

Contributors and editors

Professor Dorairajan Balasubramanian trained as a physical chemist but has been working on the biochemistry and biophysics of the blinding eye disease cataract. He is a Fellow of the American Association for Advancement of Science (AAAS). In addition to his professional research, he is also interested in taking science to the general public through his bi-weekly newspaper column on popular science and his participation in programmes of All India Radio, Doordarshan and, in particular, the countrywide classroom programme of the University Grants Commission.

Dr. Shama Barnabas obtained a Ph.D. in Biochemistry from Poona University and taught for over a decade in Ahmednagar. She joined the National Chemical Laboratory (NCL), Pune, as U.G.C. Scientist in 1984 and is now in the Division of Biochemical Sciences at NCL. She works in the area of molecular evolution, using mitochondrial DNA as an evolutionary probe to study the Indian population.

Professor André Béteille teaches Sociology in the University of Delhi and is a Fellow of the British Academy. Apart from contributing scholarly periodicals, he has published a number of books including *Caste, Class and Power* (1965), *Inequality Among Men* (1977), *Essays in Comparative Sociology* (1987) and *Society and Politics in India* (1991).

Professor Alan Holland Bittles was educated at Trinity College, University of Dublin and Queen's University, Belfast. In 1993, he took up the Foundation Chair of Human Biology at Edith Cowan University in Perth, Australia. He was awarded a ScD by Trinity, Dublin, in 1994 and was elected a Fellow of the Royal College of Pathologists in 1996.

Dr. A. Radha Rama Devi is a doctor by profession and has been working as a medical officer in the health centre of the Indian Institute of Science, Bangalore. Apart from her clinical work, she has been involved in basic research, particularly in the area of genetically related diseases and clinical symptoms. This has let her interact, collaborate and provide clinical expertise in a number of research projects involving the genetic and biochemical aspects of inheritable diseases.

Professor Madhav Dhananjaya Gadgil obtained his M.Sc. from Bombay University and Ph.D. from Harvard University where he also taught for two years. He has been

with the Indian Institute Science, Bangalore, at the Centre for Ecological Sciences since 1973. He is also an Honorary Professor and Chairman of the Biodiversity Unit of the Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore. He is a Foreign Fellow of the U.S. National Academy of Sciences, and has been a member of the Science Advisory Committee to the Prime Minister of India. He was conferred the Padma Shri by the Government of India.

Professor Niranjan Vasudeo Joshi obtained his M.Sc. from I.I.T., Mumbai, and Ph.D. from the Indian Institute of Science, Bangalore, where he is currently working at the Centre for Theoretical Studies and the Centre for Ecological Sciences. He works in the area of mathematical modelling in biology, ecology and genetics.

Professor Partha P. Majumder is associated with the Anthropology and Human Genetics Unit of the Indian Statistical Institute, Calcutta. His major interests and contributions are in genetic epidemiology and genetic structures of human populations.

Dr. S. Manoharan received his masters degree from Annamalai University and Ph.D. from the University of Calcutta for studies on Andamanese language. He has been with the Anthropological Survey of India since 1975 and has carried out extensive fieldwork among the great Andamanese and the Bhil tribes. He has to his credit, two books and about thirty papers.

Dr. Sheila Mishra is a lecturer in Geomorphology at Deccan College, Pune. Her research is mainly related to the Stone Age Prehistory and Pleistocene Palaeoenvironments.

Dr. P. Divakar Naidu received his masters degree from S.V. University in 1981 and Ph.D. from Gothenburg University, Sweden, in 1995. He joined the National Institute of Oceanography in 1982. He has published papers covering the areas of monsoons, palaeoceanography, palaeoclimate, micropalaeontology and global carbon cycles. He is currently working on the thermohaline circulation problem of the Indian Ocean.

Dr. Suresh Patil graduated in Social Anthropology from Karnataka University, Dharwad, and is now with the Anthropological Survey of India, Mysore. He was a collaborator in the multivariate analysis of the data generated under the People of India (POI) Project at the Centre for Ecological Sciences, Indian Institute of Science, Bangalore. He has also acted as the state co-ordinator for Karnataka and is the co-author of a volume on communities in Karnataka under POI.

Dr. D.P. Pattanayak received his doctorate from Cornell, and was a former Director of the Central Institute of Indian Languages. A former Jawaharlal Nehru Fellow, he has authored ten books and published about a hundred papers. He was conferred the Padma Shri by the Government of India.

U.V. Shambu Prasad is a historian and has worked on medieval migrations. He was associated with the Centre for Ecological Sciences for two years. He is currently Director (Research), Divya Jeevan Foundation, which carries out research on demography, ecological history and issues relating to tribals in northeastern India. He is also Honorary Director of Research, Centre for Research in Indo-Bangladesh Relations, Calcutta, and the Sri Aurobindo Institute of Indian Culture, Shillong.

Dr. S.N. Rajaguru retired as a Professor of Geoarcheology from Deccan College, Pune, three years ago. He has specialised in environmental archaeology, Quaternary geology and Quaternary climatic changes, especially of western India.

Professor Vulimiri Ramalingaswami is a distinguished pathologist, medical researcher and educationist, and is currently a National Research Professor of India and Professor Emeritus in the Department of Pathology at the All India Institute of Medical Sciences, New Delhi. He has served as Chairman of the WHO Advisory Committee on Medical Research and as Special Advisor to the Director-General, UNICEF. He is continuing research in the area of communicable diseases, their reduction, management and prevention. He was President of the Indian National Science Academy during 1979–80.

Professor Naropantul Appaji Rao has been with the Indian Institute of Science, Bangalore, for over three decades. He is well-known for his notable contributions to enzymology and his studies on the effects of inbreeding in human populations. A recipient of the Sreenivasayya Memorial Award and the Jagadish Chandra Bose Medal of INSA, he is currently a CSIR Emeritus Scientist at the Indian Institute of Science, Bangalore, and also a Secretary of INSA.

Dr. Handanahal Subbarao Savithri obtained her M.Sc. from Bangalore University and Ph.D. from the Indian Institute of Science, Bangalore, where she is currently an Associate Professor at the Department of Biochemistry. She was a recipient of the P.S. Sarma Memorial Award of the Society of Biological Chemists (India) for 1991. Her areas of expertise are plant virology, protein chemistry and enzymology.

Renu Saxena obtained a Ph.D. in Genetics from Osmania University, Hyderabad, and is currently in charge of the Molecular Diagnostic Laboratory at Sir Ganga Ram Hospital, New Delhi. For the past several years she has been involved in the molecular analysis and prenatal diagnosis of common genetic disorders in India such as β -thalassemia, Duchenne muscular dystrophy, spine muscular atrophy, Wilson disease, cystic fibrosis and hemophilia.

Dr. K.S. Singh, formerly of the Indian Administrative Service, has spent many years in the Jharkhand region serving and studying tribal people. He has been a recipient of many fellowships and has received awards for his writings and outstanding services to tribal communities. Among his well-known works are *Birsa Munda and his Movement* (1983), *The Indian Famine 1967: A Study in Crisis and Change* (1972), and *Tribal Society in India: An Anthro-po-historical Perspective* (1985). His *magnum opus* has been a 43-volume project on the people of India based on the first Pan-Indian survey of all communities of India, conceptualised, spearheaded, authored and edited by him, which has been described as an "enduring contribution to anthropological and sociological research in India."

Dr. B.L.K. Somayajulu is an Honorary Professor and CSIR Emeritus Scientist at the Physical Research Laboratory, Ahmedabad. His specialisation is in geochronology, geochemistry and oceanography.

Dr. C.G. Suresh obtained his masters degree in Physics from I.I.T. Chennai, D.I.I.Sc. from Bangalore and Ph.D. in Molecular Biophysics from the Indian Institute of Science, Bangalore. He is currently in the Division of Biochemical Sciences at NCL, Pune, and works in the areas of biophysics and biomolecular crystallography.

Professor Prakash Narain Tandon trained in Lucknow and at the University of London as a physician and surgeon and obtained his FRCS in 1956. His speciality is in the area of neurosciences and neurosurgery. He is a recipient of the Padma Shri and the Padma Bhushan from the Government of India. He is currently Professor Emeritus, Department of Neurosurgery, All India Institute of Medical Sciences, New Delhi. He has been President of the Indian National Science Academy during 1991–92.

Professor I.C. Verma is a Senior Consultant and Head of the Department of Medical Genetics at Sir Ganga Ram Hospital, New Delhi. He recently retired as Professor of Pediatrics and in charge of WHO Collaborating Centre in Genetics at AIIMS, New Delhi. He has been a pioneer in the field of medical genetics services in India, and has made major contributions in genetics of mental retardation, congenital malformations, molecular characterisation and prenatal diagnosis of thalassemia and muscular dystrophies in India.

Index

- α -thalassemia, 3
- β -thalassemia, 4, 8
 - carriers of, 4, 5
 - community control of, 7
 - homozygous, 4
 - molecular characterisation of, 5
 - molecular mutations causing, 5
 - prenatal diagnosis of, 6 (*see also* prenatal diagnosis)
- A. africanus*, 27
- A. robustus*, 27
- aborigines, 25
- abortion, 7
 - selective, 5
- affinities,
 - genetic, 52–55, 106
 - determinant of, 57
 - physical, 55
- African hominoids, 27
- Ahartaattva*, 24
- AIDS, 3
- All India Bio-anthropological Survey, 78
- alleles, 32, 49
- allozygosity, 12
- Alu elements, 32, 33
- Ambedkar, 98
- amino acid disorders (*see* aminoacidopathies)
- amino acidemia, 15
- amino acidopathies, 13
- amplification refractory mutation system (ARMS), 6
- ancestry, 34
- Anglo-Indians, 83
- Anthropological Survey of India (ASI), 78, 79
- anthropology, 79
- antimalarials, 25
- archaeology, 27
- artifacts, 66
 - dating, 60, 63, 67
- Aryans, 96
- Asian Indians, 5–7
- Austic speakers, 110
- auto-correlation analysis, 55
- autosomal dominant disorders, 16
- autosomal recessive disorders, 13, 16
- autosomes, 32
- autozygosity, 12
- Ayurveda*, 23, 24
- Babur, 122
- Bankimchandra, 93
- beauty, 81
- Bharat Mata*, 80
- bilingualism, 81
- biodiversity, 79
- blood transfusions, 5
- Bori tephra, 67
- Bose, N.K., 87–89
- Bose, Satyen, 97
- bow, 120
- burial styles, 116
- Burkitt, Denis, 23
- cannons, 121
- carrier testing, 5
- caste endogamy, 81
- caste structure, organisation of, 46
- Caucasians, 28, 29, 40
- cephalic index, 47
- Civilisation(s),
 - Mohenjodaro–Harappa, 81, 96, 118
 - destruction of, 73
 - Indus Valley, 72
 - decline of, 73
 - Maya,
 - collapse of, 74
- climatic fluctuations, 75
- codons, 6
- common lineage, 35
- communication, 95, 99
- communities, 80, 81, 84
 - social organisation of, 78
 - ranks of, 84
- consanguineous marriage, (*see* consanguineous union(s))
- consanguineous unions, 14, 88

- first cousins, 12, 14
- second cousins, 14
- uncle-niece, 12, 14
- consanguinity, 14
- Constitution of India, The, 83, 92, 98
- coronary heart disease, 25
- cremation, 116
- cultivation, 83, 107, 113
- cultural homogenisation, 85
- culture, 40
- D-loop (*see* displacement loop)
- data comparability, 58
- dating methods, 61, 63
- democracy, 90
- dendrogram, 35
- Department of Biotechnology, 86
- deshachar*, 90
- Dharmashastra*, 91, 92
- diseases, 2
- disorder, 91
- displacement loop, 30, 31
 - sequencing, 40
- divergence, rate of, 30, 31
- diversity, 84, 88
 - biological, 80, 100
 - cultural, 82, 122
 - genetic, 49, 55, 57
 - linguistic, 81
 - nucleotide, 34
 - physical, 55
 - religious, 89
- DNA, 5, 28, 33
 - evolution of, 28
 - heterozygous, 6
 - homozygous, 6
 - mitochondrial, 28, 30, 31, 34
 - types of, 35, 39
 - sequences, 32
- Dravidian language(s), 34, 39, 40, 108
 - origin of, 56
 - speakers of, 56
- Dravidians, 96
- Einstein, 26
- Ekman transport, 71
- epidemic, 1
- equality, 91
- ethnic units, 80
- ethnography, 79
- evidence, archaeological, 40
- evolution, 27
 - models of, 33
- excavation, 63
- fasting, 24
- food, 23, 24, 82
 - animal protein, 24
 - fibre-rich diet, 23
- fossil(s), 27, 40
- freedom, individual, 91, 92
- Gandhi, Mahatma, 22, 98
- Garden of Eden, 34
- gastric inhibitory polypeptide (GIP), 24
- gene flow, 1
- genetic disorders, 16
- genetic distance, 46
- genetic diversification, 46, 57
- genetic markers,
 - molecular, 27, 40
 - DNA, 28
- genetic polymorphism, 3
- genetic relationships, 51, 54
 - dendrogram of, 52
- genetic similarity, 54
- genetic variation, 30
- globalisation, 85
- government offices, 93
- greenhouse effect, 75
- greenhouse gases, 76
- gunpowder, 121
- handaxes, 64, 67
- Harappan script, 96
- Haviks, 124
- heterozygosity, 32, 49, 101
- high resolution site mapping studies, 31
- Hindu law, 90
- Hindu society, structure of, 90
- histocompatibility locus antigens (HLA), 28
- HIV 1 virus, 3
- HIV, 3
- Holocene, 72
- Homo erectus*, 27, 33
- Homo ergaster*, 27
- Homo sapiens*, 27, 30, 34, 40, 119
- homogeneity, 34

- homozygosity, 49
- horse, domestication of, 115
- horseshoe, 121
- hominoids, African, 27
- homogenisation, rate of, 57
- human genome, 3
- hypervariable loci, 32
- hypervariable region, 31
- ideology, 89
- immigrants,
 - Asian, 2
 - Japanese, 2
- inbreeding, 12, 13, 16, 18
 - coefficient of, 12, 13, 15
 - genetic consequences of, 13
- India, modernisation of, 87
- Indian populations, 111
- Indian Palaeoliths, 63
- Indian Statistical Institute, 52, 53
- Indian writers, 87
- Indonesia, 89
- inheritance, maternal, 29
- innovations,
 - role of, 101
 - significant, 120
 - technological, 115
- insulinotropic hormone, 24
- intercellular adhesion molecules (ICAM), 3
- intermarriage, 57
- invasions, 56
- iron, 115
 - use of, 118
- isolation, 1
 - geographic, 1
- Jinnah, 99
- Karve, Irawati, 87–89
- Kalingapattanam, 88
- language(s), 86, 97, 107, 112, 118
 - Austro-Asiatic, 39
 - Brahui, 40, 96, 114
 - Dravidian, 34, 39, 40, 108
 - Elamite, 39
 - Indo-European, 34, 39, 40
 - vernacular, 96, 97
- language families, 81, 95, 108, 110
- language heritage, 95
- language policy, 98
- linguistic families, 47 (*see also* language families)
- linguistic units, 80
- linguistic region, 82
- Little Ice Age, 101
- lokachar*, 90
- Lower Palaeolithic, 65
- magnetic reversal, 67 (*see also* palaeomagnetic reversal)
- major histocompatibility complex (MHC), 3
- malaria, 2, 3
- Manusmriti*, 92 (*see also* *Smriti*)
- markers, 58 (*see also* genetic markers)
- Marx, Karl, 98
- marriages, endogamous, 8
- mass communication, 97
- meditation, 25
- Middle Palaeolithic, 64
- Middle Pleistocene, 40
- migrant(s), 6, 39, 80, 82
 - groups, 81
- migration(s), 1, 2, 32, 33, 40, 80, 82, 101, 107, 113, 114, 120
- migration maps, 96
- minorities, 83
- Miocene, 27
- mitochondrial DNA (*see* DNA)
- modern man, 30, 40
 - African origin of, 31
 - origin of, 33
- Mongoloid, 28, 29
- monsoon, 69
 - mechanism of, 69
- mortality, 3, 12
 - data, 16
 - infection, 3
 - rate, 25
- movement, population, 56
- Mukris, 124
- multi-locus probe (MLP), 32
- mutation(s), 7, 28, 30, 36
 - causative, 6
 - common, 5
 - maternal, 7
 - rare, 6, 7
 - rate, 105

- nasal index, 48
- national movement, 87
- 'nature-nurture' interaction, 2
- Neanderthal man, 27
- nef* gene, 3
- Negroid, 28, 29
- Nehru, Jawaharlal, 23, 80, 91, 98
- neighbour joining tree, 105
- non-vegetarianism, 82
- occupation(s), 83, 84
- Ocean Drilling Program (ODP), 72
- Oldown, 64
- organisation, 90
 - family, 88
 - hierarchical, 90
- outbreeding, 13, 18, 49
- palaeomagnetic reversal, 66
- Palaeontology, 27
- pandemic, 1
 - first, 1
 - second, 2
 - third, 2
- parsimony method, 30, 31, 35
- parsimony tree, 35 (*see* tree)
- people of India, profile of, 79
- People of India Project (POI), 78, 79, 86, 108
- peopling of India, 80, 111, 120
- phylogenetic tree, 30, 34, 35, 105, 124 (*see also* tree)
- phylogenetic relationship, 35
- plague, 1, 2
- plasma insulin level, 24
- Pleistocene, 63
- plurality of norms, 92
- politico-administrative units, 80, 83
- pollen studies, 72
- polymorphic Alu insertion(s), 32, 33
- polymorphism, genetic (*see* genetic polymorphism)
- populations,
 - clustering of, 49
 - physical affinities, 49
- population movement (*see* movement)
- pottery, 113
- prenatal diagnosis, 5, 7, 8
 - β -thalassaemia, 6
- principal components (PC), 106
- Pseudocholinesterase deficiency, 18
- public institutions, 92
- Quaternary, 63
- rain, effect of, 71
- red blood cells (RBCs), 3
- religion,
 - conversion of, 52, 57
 - politically dominant, 89
- religious beliefs, 89
- repetitive DNA polymorphism, 32
- restriction endonuclease, 29
- restriction enzyme, 31
- restriction fragment length polymorphism (RFLP), 29-31
- Rio de Janeiro summit, 76
- rules, 91
 - disregard of, 92
 - new, 93
 - of conduct, 91
 - proliferation of, 92
- Sanskrit, 96, 97
- sanyasis*, 91
- scheduled castes, 78, 82, 83
- scheduled tribes, 78, 82, 83
- schizophrenia, 2
- scoline apnoea, 18
- screening,
 - antenatal, 8
 - neonatal, 13, 15
- sediment trap experiment, 72
- settled cultivation, 83 (*see also* cultivation)
- shastras*, 93
- short interspersed elements (SINEs), 32
- short tandem repeat polymorphic segment (STRP), 33
- sickle cell anaemia, 3
- single-locus probe (SLP), 32
- Smriti*, 90
- society, hierarchical, 90
- southwest (SW) monsoon,
 - intensity of, 72
- spinning wheel, 122
- stirrup, 121
- stone tool(s), 64, 67
- Th/U dating, 67 (*see also* dating methods)
- thalassaemia, 3 (*see also* β -thalassaemia)

Thalassemics India, 8
 three language formula, 97, 98
 tools, 64
 tracing ancestry, 29
 tracing patrilineage, 31
 tree,
 genealogical, 31
 parsimony, 35
 phylogenetic, 30, 34, 35, 105, 124
Unani, 23
 universities, 93
 unbiased pair group method with arithmetic
 averages (UPGMA), 31, 35

Upper Palaeolithic, 40, 65
 upwelling, 70
 indices, 72
 variable number of tandem repeats (VNTRs), 32
varnas, 90
 Vedic people, 118, 119
 vegetarianism, 82
 volcanic ash, 67
 Y chromosome, 31
Yagnyavalka, 90

The book

This book is a collection of articles by experts from different fields. While the focus of each article is different from the others, the common thread of the heritage of India strings them together to form a well-represented foray into various aspects of the Indian Human Heritage. Written by experts in their respective fields, these articles analyse the health, cultural, linguistic and sociological heritage of India. Also included are articles which look at the dating of archaeological material and assess the effects of climatic and geological changes on the Indian subcontinent as well as on ancient civilisations.

The editors

Prof. D. Balasubramanian is presently Director, Centre for Cellular and Molecular Biology, Hyderabad. He is also a Fellow of the American Association for the Advancement of Science (AAAS). In addition to his professional research on the biochemistry and biophysics of cataract, he has a keen interest in popularising science as demonstrated by his popular articles, books and educational programmes in the media. He was awarded the 1997 Kalinga Award for his contributions to the popularisation of science.

Prof. N. Appaji Rao has been with the Indian Institute of Science, Bangalore, for over three decades and is well-known for his notable contributions to enzymology and his studies on the effects of inbreeding in human populations. A recipient of the Sreenivasayya Memorial Award and the Jagadish Chandra Bose Medal, he is currently a CSIR Emeritus Scientist and a Secretary of the Indian National Science Academy (INSA).

Cover design: OSDATA

Rs 325.00



Universities Press

Balasubramanian & Appaji Rao: *The Indian Human Heritage*